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Date completed: 07-16-02
Searcher: Beverly C4994
Terminal time: 29
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Number of Searches: _____
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_____ DARC/Questel
✓ Other CGN

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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 07:19:07 ; Search time 1859.7 Seconds
(without alignments)
236.305 Million cell updates/sec

Title: US-09-981-606-15
Perfect score: 21
Sequence: 1 gtgtggagcctcaacatcctg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
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14: gb_vi:*
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19: em_mu:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	10825	6	AR117789	AR117789 Sequence
2	21	100.0	10825	6	AR117790	AR117790 Sequence
3	21	100.0	10825	6	AR117791	AR117791 Sequence
4	21	100.0	10825	6	AR117792	AR117792 Sequence
5	21	100.0	10825	6	AR149459	AR149459 Sequence
6	21	100.0	10825	6	AR149460	AR149460 Sequence
7	21	100.0	10825	6	AR149461	AR149461 Sequence
8	21	100.0	10825	6	AR149462	AR149462 Sequence
9	21	100.0	12146	9	HSHFE	Z92910 Homo sapien
c 10	21	100.0	193752	2	AL359892	AL359892 Homo sapi
11	21	100.0	246240	6	AR036572	AR036572 Sequence
12	21	100.0	246240	6	AR036573	AR036573 Sequence
13	21	100.0	246240	6	AR036574	AR036574 Sequence
c 14	21	100.0	246282	9	HSU91328	U91328 Human hered
c 15	18	85.7	160671	9	AC090451	AC090451 Homo sapi
16	18	85.7	169059	9	AC009514	AC009514 Homo sapi
17	18	85.7	181381	2	AC087856	AC087856 Homo sapi
18	17.8	84.8	37193	2	AC079928	AC079928 Homo sapi
c 19	17.8	84.8	143690	9	AL356252	AL356252 Human DNA
c 20	17.8	84.8	155827	2	AC104172	AC104172 Homo sapi
c 21	17.8	84.8	162217	9	AC068043	AC068043 Homo sapi
c 22	17.8	84.8	178617	2	AC021529	AC021529 Homo sapi
23	17.8	84.8	180548	9	AL596223	AL596223 Human DNA
c 24	17.8	84.8	182435	9	AC096591	AC096591 Homo sapi
c 25	17.4	82.9	135369	2	AC090557	AC090557 Homo sapi
26	17.4	82.9	149143	2	AC092974	AC092974 Homo sapi
27	17.4	82.9	150887	2	AC018580	AC018580 Homo sapi
c 28	17.4	82.9	158543	2	AC024413	AC024413 Homo sapi
c 29	17.4	82.9	163357	2	AC023276	AC023276 Homo sapi
c 30	17.4	82.9	173310	2	AC090454	AC090454 Homo sapi
c 31	17.4	82.9	175517	9	AL162385	AL162385 Human DNA
c 32	17.4	82.9	181923	9	AC022872	AC022872 Homo sapi
c 33	17.4	82.9	184513	2	AC024433	AC024433 Homo sapi
c 34	17.4	82.9	185596	2	AC093007	AC093007 Homo sapi
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c 36	17.4	82.9	197419	8	ATCHRIV41	AL161541 Arabidops
c 37	16.8	80.0	42398	9	D84401	D84401 Homo sapien
38	16.8	80.0	44090	9	AC000080	AC000080 Homo sapi
c 39	16.8	80.0	64722	2	AC100765	AC100765 Homo sapi
c 40	16.8	80.0	67401	9	MMU421778	AJ421778 Macaca mu
41	16.8	80.0	67895	9	AL138807	AL138807 Human DNA
42	16.8	80.0	68152	2	AC102891	AC102891 Mus muscu
c 43	16.8	80.0	68152	2	AC102891	AC102891 Mus muscu
c 44	16.8	80.0	69135	2	AC102100	AC102100 Mus muscu
45	16.8	80.0	70069	2	AC037477	AC037477 Homo sapi

ALIGNMENTS

RESULT 1
AR117789
LOCUS AR117789 10825 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6140305.
ACCESSION AR117789
VERSION AR117789.1 GI:14098695
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 10825)
AUTHORS Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D., Tsuchihashi,Z. and Wolff,R.K.
TITLE Hereditary hemochromatosis gene products
JOURNAL Patent: US 6140305-A 1 31-OCT-2000;
FEATURES Location/Qualifiers
source 1. .10825
/organism="unknown"
BASE COUNT 2998 a 2253 c 2648 g 2926 t
ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 10825;

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Db   3695 GTGTGGAGCCTCAACATCCTG 3715


RESULT   2
AR117790
LOCUS       AR117790               10825 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 3 from patent US 6140305.
ACCESSION   AR117790
VERSION     AR117790.1  GI:14098696
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10825)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Hereditary hemochromatosis gene products
  JOURNAL   Patent: US 6140305-A 3 31-OCT-2000;
FEATURES             Location/Qualifiers
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Qy      1 gtgtggagcctcaacatcctg 21
          |||||||||||||||||||||
Db   3695 GTGTGGAGCCTCAACATCCTG 3715


RESULT   3
AR117791
LOCUS       AR117791               10825 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 5 from patent US 6140305.
ACCESSION   AR117791
VERSION     AR117791.1  GI:14098697
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10825)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Hereditary hemochromatosis gene products
  JOURNAL   Patent: US 6140305-A 5 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .10825
                     /organism="unknown"
BASE COUNT     2998 a   2252 c   2649 g   2926 t
ORIGIN


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Qy      1 gtgtggagcctcaacatcctg 21
          |||||||||||||||||||||
Db   3695 GTGTGGAGCCTCAACATCCTG 3715


RESULT   4
AR117792
LOCUS       AR117792               10825 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 7 from patent US 6140305.
ACCESSION   AR117792
VERSION     AR117792.1  GI:14098698
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10825)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Hereditary hemochromatosis gene products
  JOURNAL   Patent: US 6140305-A 7 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .10825
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BASE COUNT     2999 a   2252 c   2648 g   2926 t
ORIGIN


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Qy      1 gtgtggagcctcaacatcctg 21
          |||||||||||||||||||||
Db   3695 GTGTGGAGCCTCAACATCCTG 3715


RESULT   5
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LOCUS       AR149459               10825 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6228594.
ACCESSION   AR149459
VERSION     AR149459.1  GI:15114050
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10825)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Method for determining the presence or absence of a hereditary
            hemochromatosis gene mutation
  JOURNAL   Patent: US 6228594-A 1 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .10825
                     /organism="unknown"
BASE COUNT     2998 a   2253 c   2648 g   2926 t
ORIGIN


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          |||||||||||||||||||||
Db   3695 GTGTGGAGCCTCAACATCCTG 3715


RESULT   6
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LOCUS       AR149460               10825 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 3 from patent US 6228594.
ACCESSION   AR149460
VERSION     AR149460.1  GI:15114051
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10825)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
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  TITLE     Method for determining the presence or absence of a hereditary
            hemochromatosis gene mutation
  JOURNAL   Patent: US 6228594-A 3 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .10825
                     /organism="unknown"
BASE COUNT     2999 a   2253 c   2647 g   2926 t
ORIGIN
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Qy      1 gtgtggagcctcaacatcctg 21
          |||||||||||||||||||||
Db   3695 GTGTGGAGCCTCAACATCCTG 3715
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RESULT   7
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LOCUS       AR149461                10825 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 5 from patent US 6228594.
ACCESSION   AR149461
VERSION     AR149461.1  GI:15114052
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10825)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Method for determining the presence or absence of a hereditary
            hemochromatosis gene mutation
  JOURNAL   Patent: US 6228594-A 5 08-MAY-2001;
FEATURES             Location/Qualifiers
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BASE COUNT     2998 a   2252 c   2649 g   2926 t
ORIGIN
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Qy      1 gtgtggagcctcaacatcctg 21
          |||||||||||||||||||||
Db   3695 GTGTGGAGCCTCAACATCCTG 3715
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RESULT   8
AR149462
LOCUS       AR149462                10825 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 7 from patent US 6228594.
ACCESSION   AR149462
VERSION     AR149462.1  GI:15114053
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10825)
  AUTHORS   Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
            Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Method for determining the presence or absence of a hereditary
            hemochromatosis gene mutation
  JOURNAL   Patent: US 6228594-A 7 08-MAY-2001;
FEATURES             Location/Qualifiers
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ORIGIN
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Qy      1 gtgtggagcctcaacatcctg 21
          |||||||||||||||||||||
Db   3695 GTGTGGAGCCTCAACATCCTG 3715
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RESULT   9
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LOCUS       HSHFE                   12146 bp    DNA     linear   PRI 23-JUL-1999
DEFINITION  Homo sapiens HFE gene.
ACCESSION   Z92910
VERSION     Z92910.1  GI:1890179
KEYWORDS    haemochromatosis; HFE gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 858)
  AUTHORS   Albig,W., Drabent,B., Burmester,N., Bode,C. and Doenecke,D.
  TITLE     The haemochromatosis candidate gene HFE (HLA-H) of man and mouse is
            located in syntenic regions within the histone gene cluster
  JOURNAL   J. Cell. Biochem. 69 (2), 117-126 (1998)
  MEDLINE   98208340
REFERENCE   2  (bases 1 to 12146)
  AUTHORS   Albig,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-MAR-1997) Albig W., Georg-August-Universitaet
            Goettingen, Biochemie und Molekulare Zellbiologie, Humboldtallee
            23, Goettingen, FRG, 37073
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /clone_lib="ICRF YAC-library"
     exon            1028. .1324
                     /gene="HFE"
                     /number=1
     gene            1028. .10637
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                     6928. .7041,7995. .8035)
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                     /function="iron metabolism"
                     /note="haemochromatosis candidate gene"
                     /codon_start=1
                     /protein_id="CAB07442.1"
                     /db_xref="GI:1890180"
                     /db_xref="SWISS-PROT:Q30201"
                     /translation="MGPRARPALLLLMLLQTAVLQGRLLRSHSLHYLFMGASEQDLGL
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                     /rpt_family="Alu"
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     intron          5401. .6493
                     /gene="HFE"
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     exon            6494. .6769
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     intron          6770. .6927
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ORIGIN


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Qy       1 gtgtggagcctcaacatcctg 21
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Db    4585 GTGTGGAGCCTCAACATCCTG 4605


RESULT 10
AL359892/c
LOCUS       AL359892               193752 bp    DNA     linear   HTG 13-JUN-2001
DEFINITION  Homo sapiens chromosome 6 clone RP11-557F22, *** SEQUENCING IN
            PROGRESS ***, 18 unordered pieces.
ACCESSION   AL359892
VERSION     AL359892.5  GI:9930971
KEYWORDS    HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 193752)
  AUTHORS   Sims,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Aug 27, 2000 this sequence version replaced gi:9864230.
            -------------- Genome Center
            Center: Sanger Centre
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------- Project Information
            Center project name: bA557F22
            -------------- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Consensus quality: 183925 bases at least Q40
            Consensus quality: 187703 bases at least Q30
            Consensus quality: 189658 bases at least Q20
            Insert size: 192052; sum-of-contigs
            Insert size: 198247; agarose-fp
            Quality coverage: 3.68x in Q20 bases; sum-of-contigs Quality
            coverage: 3.70x in Q20 bases; agarose-fp
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 18 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     3250: contig of 3250 bp in length
            *     3251  3350: gap of      100 bp
            *     3351    14600: contig of 11250 bp in length
            *    14601  14700: gap of      100 bp
            *    14701    32357: contig of 17657 bp in length
            *    32358  32457: gap of      100 bp
            *    32458    34886: contig of 2429 bp in length
            *    34887  34986: gap of      100 bp
            *    34987    43490: contig of 8504 bp in length
            *    43491  43590: gap of      100 bp
            *    43591    47437: contig of 3847 bp in length
            *    47438  47537: gap of      100 bp
            *    47538    57356: contig of 9819 bp in length
            *    57357  57456: gap of      100 bp
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            *   158760   164235: contig of 5476 bp in length
            *   164236 164335: gap of      100 bp
            *   164336   184996: contig of 20661 bp in length
            *   184997 185096: gap of      100 bp
            *   185097   193752: contig of 8656 bp in length.
FEATURES             Location/Qualifiers
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ORIGIN


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Db  12957 GTGTGGAGCCTCAACATCCTG 12937


RESULT  11
AR036572
LOCUS       AR036572              246240 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 20 from patent US 5872237.
ACCESSION   AR036572
VERSION     AR036572.1  GI:5953240
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 246240)
  AUTHORS   Feder,J.Nathan., Kronmal,G.Scott., Lauer,P.M., Ruddy,D.A.,
            Thomas,W., Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Megabase transcript map: novel sequences and antibodies thereto
  JOURNAL   Patent: US 5872237-A 20 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .246240
                     /organism="unknown"
BASE COUNT    73211 a  50177 c  50599 g  72252 t      1 others
ORIGIN


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  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtgtggagcctcaacatcctg 21
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Db 195998 GTGTGGAGCCTCAACATCCTG 196018


RESULT  12
AR036573
LOCUS       AR036573              246240 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 21 from patent US 5872237.
ACCESSION   AR036573
VERSION     AR036573.1  GI:5953241
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 246240)
  AUTHORS   Feder,J.Nathan., Kronmal,G.Scott., Lauer,P.M., Ruddy,D.A.,
            Thomas,W., Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Megabase transcript map: novel sequences and antibodies thereto
  JOURNAL   Patent: US 5872237-A 21 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .246240
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BASE COUNT    73211 a  50177 c  50599 g  72252 t      1 others
ORIGIN


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  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtgtggagcctcaacatcctg 21
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Db 195998 GTGTGGAGCCTCAACATCCTG 196018


RESULT  13
AR036574
LOCUS       AR036574              246240 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 22 from patent US 5872237.
ACCESSION   AR036574
VERSION     AR036574.1  GI:5953242
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 246240)
  AUTHORS   Feder,J.Nathan., Kronmal,G.Scott., Lauer,P.M., Ruddy,D.A.,
            Thomas,W., Tsuchihashi,Z. and Wolff,R.K.
  TITLE     Megabase transcript map: novel sequences and antibodies thereto
  JOURNAL   Patent: US 5872237-A 22 16-FEB-1999;
FEATURES             Location/Qualifiers
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BASE COUNT    73211 a  50177 c  50599 g  72252 t      1 others
ORIGIN


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Qy      1 gtgtggagcctcaacatcctg 21
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Db 195998 GTGTGGAGCCTCAACATCCTG 196018

RESULT 14
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LOCUS HSU91328 246282 bp DNA linear PRI 17-DEC-2001
DEFINITION Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.
ACCESSION U91328
VERSION U91328.1 GI:2088550
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 246282)
AUTHORS Ruddy,D.A., Kronmal,G.S., Lee,V.K., Mintier,G.A., Quintana,L., Domingo,R. Jr., Meyer,N.C., Irrinki,A., McClelland,E.E., Fullan,A., Mapa,F.A., Moore,T., Thomas,W., Loeb,D.B., Harmon,C., Tsuchihashi,Z., Wolff,R.K., Schatzman,R.C. and Feder,J.N.
TITLE A 1.1-Mb transcript map of the hereditary hemochromatosis locus
JOURNAL Genome Res. 7 (5), 441-456 (1997)
MEDLINE 97294057
PUBMED 9149941
REFERENCE 2 (bases 1 to 246282)
AUTHORS Ruddy,D.A., Kronmal,G.S., Lee,V.K., Mintier,G.A., Quintana,L., Domingo,R. Jr., Meyer,N.C., Irrinke,A., McClelland,E., Fullan,A., Mapa,F.A., Moore,T., Thomas,W., Loeb,D.B., Harmon,C., Tsuchihashi,Z., Wolff,R.K., Schatzman,R.C. and Feder,J.N.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1997) Sequencing, Mercator Genetics, 4040 Campbell Avenue, Menlo Park, CA 94025, USA

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	/rpt_type=dispersed
repeat_region	34235. .34314
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Qy       1 gtgtggagcctcaacatcctg 21
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RESULT 15
AC090451/c
LOCUS       AC090451              160671 bp    DNA     linear   PRI 31-JAN-2002
DEFINITION  Homo sapiens chromosome 8, clone RP11-318N11, complete sequence.
ACCESSION   AC090451
VERSION     AC090451.6  GI:18252721
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 160671)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 8, clone RP11-318N11
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 160671)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A.,
            Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
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            Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
            Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-FEB-2001) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 160671)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
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            Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
            Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JAN-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Jan 21, 2002 this sequence version replaced gi:15144524.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L10556
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Center clone name: 318_N_11

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Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   33359 TGGAGCCTCAACATCCTG 33342
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Search completed: July 16, 2002, 09:52:19
Job time: 9192 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 07:33:27 ; Search time 273.56 Seconds
(without alignments)
131.800 Million cell updates/sec

Title: US-09-981-606-15
Perfect score: 21
Sequence: 1 gtgtggagcctcaacatcctg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	21	100.0	21	21	AAA96782	PCR primer for his
	2	21	100.0	10825	18	AAT96690	Hereditary haemoch
	3	21	100.0	10825	22	AAC68425	Human hereditary h
	4	21	100.0	10825	22	AAC68426	Human hereditary h
	5	21	100.0	10825	22	AAC68427	Human hereditary h
	6	21	100.0	10825	22	AAC68428	Human hereditary h
	7	21	100.0	12146	21	AAA96794	Genomic DNA of a h
c	8	21	100.0	237326	19	AAV57903	Hereditary haemoch
	9	17.4	82.9	3056	21	AAC42758	Arabidopsis thalia
	10	16.8	80.0	1001	21	AAC57733	Arachidonic acid m
	11	16.8	80.0	1001	21	AAC57734	Arachidonic acid m
c	12	16.8	80.0	32249	22	ABA15833	Human nervous syst
c	13	16.8	80.0	32249	22	AAL03071	Human reproductive
	14	16.4	78.1	211	21	AAC29479	Human secreted pro
	15	16.4	78.1	246	21	AAC25147	Human secreted pro
	16	16.4	78.1	323	23	AAS82234	DNA encoding novel
	17	16.4	78.1	420	22	AAI83809	Human polynucleoti
c	18	16.4	78.1	1045	22	AAK78083	Human immune/haema
c	19	16.4	78.1	1045	22	AAK84813	Human immune/haema
	20	16.4	78.1	2267	23	ABL25420	Drosophila melanog
	21	16.4	78.1	11006	22	AAK66281	Human immune/haema
c	22	16.4	78.1	17245	22	AAK83897	Human immune/haema
	23	16.4	78.1	32212	22	AAL06082	Human reproductive
c	24	16.4	78.1	43938	22	AAK77216	Human immune/haema
c	25	16.4	78.1	45017	22	AAK77217	Human immune/haema
c	26	16.4	78.1	325791	22	AAS43104	Human Oestrogen re
c	27	16.2	77.1	276	21	AAC09450	Human secreted pro
	28	16.2	77.1	1512	22	AAH32572	Human secreted pro
c	29	16.2	77.1	1512	23	ABL07285	Drosophila melanog
c	30	16.2	77.1	1778	22	AAF54816	Nucleotide sequenc
	31	16.2	77.1	2209	23	ABL12347	Drosophila melanog
	32	16.2	77.1	2633	23	ABL12345	Drosophila melanog
	33	16.2	77.1	3478	22	AAH32530	Human secreted pro
	34	16.2	77.1	3479	22	AAS21305	Human cDNA sequenc
c	35	16.2	77.1	3512	23	ABL07284	Drosophila melanog
c	36	16.2	77.1	3569	22	AAH99528	Human protein enco
	37	16.2	77.1	5787	23	ABL12346	Drosophila melanog
	38	16.2	77.1	5803	23	ABL12344	Drosophila melanog
	39	16	76.2	31	21	AAZ24187	Human BRCA2 primer
	40	16	76.2	2964	23	AAS89487	DNA encoding novel
	41	15.8	75.2	156	21	AAC14456	Human secreted pro
c	42	15.8	75.2	252	22	AAL12405	Human breast cance
c	43	15.8	75.2	252	22	AAL21281	Human breast cance
c	44	15.8	75.2	274	15	AAQ55165	Sequence from HIV-
c	45	15.8	75.2	346	22	AAL36264	Human musculoskele

ALIGNMENTS

RESULT 1
AAA96782
ID AAA96782 standard; DNA; 21 BP.
XX
AC AAA96782;
XX
DT 19-FEB-2001 (first entry)
XX
DE PCR primer for histocompatibility iron loading (HFE) gene exon 2.
XX
KW Human; histocompatibility iron loading protein; HFE protein;
KW major histocompatibility complex; non-classical class I gene;
KW chromosome 6p; iron disorder; haemochromatosis; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200058515-A1.
XX
PD 05-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US07982.
XX
PR 26-MAR-1999; 99US-0277457.
XX
PA (BILL-) BILLUPS-ROTHENBERG INC.
XX
PI Rothenberg BE, Sawada-Hirai R, Barton JC;
XX
DR WPI; 2000-647244/62.
XX
PT Diagnosing an iron disorder e.g. hemochromatosis or a genetic
PT susceptibility to develop it, by determining the presence of a mutation

```
PT   in exon 2 or an intron of a histocompatibility iron loading nucleic
PT   acid -
XX
PS   Claim 24; Page 5; 55pp; English.
XX
CC   PCR primers A96782-83 were used to amplify a fragment of the human
CC   histocompatibility iron loading (HFE) gene. The HFE gene is a major
CC   histocompatibility (MHC) non-classical class I gene located on
CC   chromosome 6p. Mutations in the gene lead to iron disorders. The
CC   specification describes a method for diagnosing an iron disorder or a
CC   genetic susceptibility to develop the disorder in a mammal. The method
CC   comprises determining the presence of a mutation in exon 2 or an intron
CC   of a HFE gene or protein. The mutation is not a C to G missense mutation
CC   at nucleotide 187 of the sequence given in A96769 (Genbank Accession
CC   number U60319). The presence of the mutation indicates the disorder or
CC   the genetic susceptibility to the disorder. The method is used to
CC   diagnose an iron disorder e.g. haemochromatosis, or a genetic
CC   susceptibility to develop it.
XX
SQ   Sequence 21 BP; 4 A; 6 C; 6 G; 5 T; 0 other;


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  Best Local Similarity   100.0%;  Pred. No. 0.59;
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Db       1 gtgtggagcctcaacatcctg 21


RESULT   2
AAT96690
ID   AAT96690 standard; DNA; 10825 BP.
XX
AC   AAT96690;
XX
DT   14-APR-1998  (first entry)
XX
DE   Hereditary haemochromatosis gene.
XX
KW   Hereditary haemochromatosis; metal toxicity; diagnosis;
KW   gene therapy; prenatal screening; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag= a
FT                   /note= "contains introns"
FT   intron          437..3761
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FT                   /number= 1
FT   intron          4026..4234
FT                   /*tag= c
FT                   /number= 2
FT   intron          4511..5605
FT                   /*tag= d
FT                   /number= 3
FT   intron          5882..6039
FT                   /*tag= e
FT                   /number= 4
FT   intron          6154..7106
FT                   /*tag= f
FT                   /number= 5
FT   mutation        3872
FT                   /*tag= g
FT                   /note= "C to G substitution (24d2 mutation)
FT                          results in His to Asp substitution"
FT   variation       3878
FT                   /*tag= h
FT                   /note= "A to T substitution (24d7 variant)
FT                          results in Ser to Cys substitution"
FT   mutation        5834
FT                   /*tag= i
FT                   /note= "G to A substitution (24d1 mutation
FT                          associated with HH), results in Cys to
FT                          Tyr substitution"
XX
PN   WO9738137-A1.
XX
PD   16-OCT-1997.
XX
PF   04-APR-1997;   97WO-US06254.
XX
PR   23-MAY-1996;   96US-0652265.
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
XX
PA   (MERC-) MERCATOR GENETICS INC.
XX
PI   Drayna DT,  Feder JN,  Gnirke A,  Ruddy D,  Thomas WJ;
PI   Tsuchihashi Z,  Wolff RK;
XX
DR   WPI; 1997-512743/47.
DR   P-PSDB; AAW36499.
XX
PT   Hereditary haemochromatosis gene and variants - useful for diagnosis
PT   and treatment of hereditary haemochromatosis disease
XX
PS   Disclosure; Fig 3; 115pp; English.
XX
CC   This genomic DNA sequence corresponds to the human gene whose
CC   mutated form is associated with hereditary haemochromatosis (HH).
CC   To identify this novel gene, allelic association patterns were
CC   determined between known markers and the HH locus in the HLA region
CC   of chromosome 6.  A physical clone coverage was then generated
CC   extending from D6S265, which is a marker that is centromeric of
CC   HLA-A, in a telomeric direction through D6S276, a marker at which
CC   the allelic association was no longer observed.  A single mutation
CC   (24d1) in the HH gene appears responsible for the majority of HH
CC   disease.  This comprises a G to A substitution that is present in
CC   86% of affected chromosomes and in 4% of unaffected chromosomes.
CC   It results in a Cys to Tyr substitution in the encoded protein (see
CC   AAW36499) at a critical disulphide bridge important for secondary
CC   structure.  The following are claimed: the HH genomic DNA (I), a
CC   1437 bp cDNA sequence (Ia) (see AAT96691) and their 24d1, 24d2 and
CC   24d7 variants; a cloning or expression vector; host cells; a
CC   peptide product chosen from the HH gene product, its variants
CC   (24d1, 24d2 and 24d7), or a peptide of at least 56 amino acid
CC   residues of these; an antibody produced using the peptide; a method
CC   to determine the presence or absence of the common HH gene
CC   mutation; an animal model for the HH disease; metal chelation
CC   agents, T-cell differentiation factors and therapeutic agents for
CC   the mitigation of injury due to oxidative process in vivo or
CC   mitigation of iron overload; a method for screening potential
CC   therapeutic agents for activity in connection with HH disease; an
CC   antisense oligonucleotide directed against a transcriptional
CC   product of a nucleic acid sequence as above; and oligonucleotides
CC   or pairs of oligonucleotides covering a range of nucleotides from
CC   (I), (Ia) or their variants, useful for detecting a polymorphism in
CC   the HH gene.  The invention also relates to methods for screening
CC   for HH homozygotes, to HH diagnosis, prenatal screening and
CC   diagnosis, and therapies of HH disease, including gene therapy,
CC   protein- and antibody-based therapeutics, and small molecule
CC   therapeutics.
XX
SQ   Sequence 10825 BP; 2996 A; 2254 C; 2648 G; 2927 T; 0 other;


  Query Match             100.0%;  Score 21;  DB 18;  Length 10825;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db   3695 gtgtggagcctcaacatcctg 3715


RESULT   3
AAC68425
ID   AAC68425 standard; DNA; 10825 BP.
XX
AC   AAC68425;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis DNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ds.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
DR   P-PSDB; AAB36869.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Fig 3; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 10825 BP; 2998 A; 2253 C; 2648 G; 2926 T; 0 other;


  Query Match             100.0%;  Score 21;  DB 22;  Length 10825;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtgtggagcctcaacatcctg 21
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Db   3695 gtgtggagcctcaacatcctg 3715


RESULT   4
AAC68426
ID   AAC68426 standard; DNA; 10825 BP.
XX
AC   AAC68426;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis 24d1 mutation DNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ds.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
PI   Thomas WJ,  Drayna DT,  Gnirke A,  Ruddy D,  Tsuchihashi Z,  Wolff RK;
PI   Feder JN;
XX
DR   WPI; 2001-006341/01.
DR   P-PSDB; AAB36870.
XX
PT   New hereditary hemochromatosis gene products or polypeptides, useful
PT   for treating hereditary hemochromatosis in a patient, and as a metal
PT   chelation agent alleviating iron overload -
XX
PS   Disclosure; Fig 3; 108pp; English.
XX
CC   The present invention relates to hereditary hemochromatosis gene
CC   products. These proteins may be used to treat a patient diagnosed as
CC   having human hemochromatosis disease. It is also useful as a metal
CC   chelation agent or as a T-cell differentiation factor, and for
CC   alleviating iron overload. They may also be used in protein replacement
CC   therapy for individuals having a defective human hemochromatosis gene.
XX
SQ   Sequence 10825 BP; 2999 A; 2253 C; 2647 G; 2926 T; 0 other;


  Query Match             100.0%;  Score 21;  DB 22;  Length 10825;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtgtggagcctcaacatcctg 21
          |||||||||||||||||||||
Db   3695 gtgtggagcctcaacatcctg 3715


RESULT   5
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ID   AAC68427 standard; DNA; 10825 BP.
XX
AC   AAC68427;
XX
DT   21-FEB-2001  (first entry)
XX
DE   Human hereditary hemochromatosis 24d2 mutation DNA.
XX
KW   HH; hereditary hemochromatosis; chelation agent;
KW   T-cell differentiation factor; iron overload; ds.
XX
OS   Homo sapiens.
XX
PN   US6140305-A.
XX
PD   31-OCT-2000.
XX
PF   04-APR-1997;   97US-0834497.
XX
PR   04-APR-1996;   96US-0630912.
PR   16-APR-1996;   96US-0632673.
PR   23-MAY-1996;   96US-0652265.
XX
PA   (BIRA ) BIO-RAD LAB INC.
XX
```

PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX
DR WPI; 2001-006341/01.
DR P-PSDB; AAB36871.
XX
PT New hereditary hemochromatosis gene products or polypeptides, useful
PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -
XX
PS Disclosure; Fig 3; 108pp; English.
XX
CC The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene.
XX
SQ Sequence 10825 BP; 2998 A; 2252 C; 2649 G; 2926 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 10825;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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||||||||||||||||||||
Db 3695 gtgtggagcctcaacatcctg 3715

RESULT 6
AAC68428
ID AAC68428 standard; DNA; 10825 BP.
XX
AC AAC68428;
XX
DT 21-FEB-2001 (first entry)
XX
DE Human hereditary hemochromatosis 24d1/2 mutation DNA.
XX
KW HH; hereditary hemochromatosis; chelation agent;
KW T-cell differentiation factor; iron overload; ds.
XX
OS Homo sapiens.
XX
PN US6140305-A.
XX
PD 31-OCT-2000.
XX
PF 04-APR-1997; 97US-0834497.
XX
PR 04-APR-1996; 96US-0630912.
PR 16-APR-1996; 96US-0632673.
PR 23-MAY-1996; 96US-0652265.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX
DR WPI; 2001-006341/01.
DR P-PSDB; AAB36872.
XX
PT New hereditary hemochromatosis gene products or polypeptides, useful
PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -
XX
PS Disclosure; Fig 3; 108pp; English.
XX
CC The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene.
XX
SQ Sequence 10825 BP; 2999 A; 2252 C; 2648 G; 2926 T; 0 other;

Query Match 100.0%; Score 21; DB 22; Length 10825;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtggagcctcaacatcctg 21
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Db 3695 gtgtggagcctcaacatcctg 3715

RESULT 7
AAA96794
ID AAA96794 standard; cDNA; 12146 BP.
XX
AC AAA96794;
XX
DT 19-FEB-2001 (first entry)
XX
DE Genomic DNA of a histocompatibility iron loading (HFE) gene.
XX
KW Human; histocompatibility iron loading protein; HFE protein;
KW major histocompatibility complex; non-classical class I gene;
KW chromosome 6p; iron disorder; haemochromatosis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT exon 1028..1324
FT /*tag= a
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PD 05-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US07982.
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PR 26-MAR-1999; 99US-0277457.
XX
PA (BILL-) BILLUPS-ROTHENBERG INC.
XX
PI Rothenberg BE, Sawada-Hirai R, Barton JC;
XX
DR WPI; 2000-647244/62.
XX
PT Diagnosing an iron disorder e.g. hemochromatosis or a genetic
PT susceptibility to develop it, by determining the presence of a mutation
PT in exon 2 or an intron of a histocompatibility iron loading nucleic
PT acid -
XX
PS Example 1; Page 21-28; 55pp; English.
XX
CC The present sequence represents the human histocompatibility iron
CC loading (HFE) gene. The HFE gene is a major histocompatibility (MHC)
CC non-classical class I gene located on chromosome 6p. Mutations in the
CC gene lead to iron disorders. The specification describes a method for
CC diagnosing an iron disorder or a genetic susceptibility to develop the
CC disorder in a mammal. The method comprises determining the presence of
CC a mutation in exon 2 or an intron of a HFE gene or protein. The mutation
CC is not a C to G missense mutation at nucleotide 187 of the sequence
CC given in A96769 (Genbank Accession number U60319). The presence of the
CC mutation indicates the disorder or the genetic susceptibility to the
CC disorder. The method is used to diagnose an iron disorder
CC e.g. haemochromatosis, or a genetic susceptibility to develop it.
XX
SQ Sequence 12146 BP; 3383 A; 2474 C; 2911 G; 3378 T; 0 other;

Query Match 100.0%; Score 21; DB 21; Length 12146;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtggagcctcaacatcctg 21
||||||||||||||||||||
Db 4585 gtgtggagcctcaacatcctg 4605

RESULT 8
AAV57903/c
ID AAV57903 standard; DNA; 237326 BP.
XX
AC AAV57903;
XX
DT 21-DEC-1998 (first entry)
XX
DE Hereditary haemochromatosis subregion from an HH affected individual.
XX
KW Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE;
KW diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3;
KW BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
KW type 1 sodium transport gene; ss.
XX
OS Homo sapiens.
XX
PN WO9814466-A1.
XX
PD 09-APR-1998.
XX
PF 30-SEP-1997; 97WO-US17658.
XX
PR 07-MAY-1997; 97US-0852495.
PR 01-OCT-1996; 96US-0724394.
XX
PA (PROG-) PROGENTIOR INC.
XX
PI Feder JN, Kronmal GS, Lauer PM, Ruddy DA, Thomas WJ;
PI Tsuchihashi Z, Wolff RK;
XX
DR WPI; 1998-240014/21.
XX
PT Hereditary haemochromatosis gene products - used to develop products
PT for the diagnosis and treatment of hereditary disorders in iron
PT metabolism
XX
PS Claim 1; Fig 9; 209pp; English.
XX
CC The present invention describes hereditary haemochromatosis gene
CC products from the human haemochromatosis gene. The present sequence
CC represents a hereditary haemochromatosis subregion from an hereditary
CC haemochromatosis (HH) affected individual. Also described is a
CC method to determine the presence or absence of the common hereditary
CC haemochromatosis (HFE) gene mutation in an individual comprising:
CC (a) providing DNA or RNA from the individual; and (b) assessing the
CC DNA or RNA for the presence or absence of a haplotype or genotype where
CC the presence or absence of the haplotype genotype indicates the likely
CC presence of the HFE gene mutation in the genome of the individual. The
CC HFE gene sequences from the present invention can be used to develop
CC products for use in the diagnosis and treatment of HFE. The present
CC invention also describes BTF genes, which are homologues of the milk
CC protein butyrophilin (BT), and can be used in the production of agonists
CC and antagonists of BT function. Also described are: (1) a RoRet gene
CC which can be used to develop products for the study, diagnosis and
CC treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes
CC which are homologues of a type 1 sodium transport gene, and can
CC similarly be used for hypophosphatemia.
XX
SQ Sequence 237326 BP; 69596 A; 48904 C; 48217 G; 70609 T; 0 other;

Query Match 100.0%; Score 21; DB 19; Length 237326;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtgtggagcctcaacatcctg 21
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Db 43405 GTGTGGAGCCTCAACATCCTG 43385

RESULT 9
AAC42758
ID AAC42758 standard; DNA; 3056 BP.
XX
AC AAC42758;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 36742.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
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PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.

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PR 21-APR-1999; 99US-0130449.
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PR 28-APR-1999; 99US-0131449.
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PR 18-JUN-1999; 99US-0139459.
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PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
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PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
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PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
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PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
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PR 04-OCT-1999; 99US-0157117.
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PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.

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PR   13-OCT-1999;   99US-0159295.
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PR   14-OCT-1999;   99US-0159331.
PR   14-OCT-1999;   99US-0159637.
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PR   21-OCT-1999;   99US-0160768.
PR   21-OCT-1999;   99US-0160770.
PR   21-OCT-1999;   99US-0160814.
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PR   22-OCT-1999;   99US-0160980.
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PR   25-OCT-1999;   99US-0161404.
PR   25-OCT-1999;   99US-0161405.
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PR   26-OCT-1999;   99US-0161361.
PR   28-OCT-1999;   99US-0161920.
PR   28-OCT-1999;   99US-0161992.
PR   28-OCT-1999;   99US-0161993.
PR   29-OCT-1999;   99US-0162142.

  Query Match             82.9%;  Score 17.4;  DB 21;  Length 3056;
  Best Local Similarity   94.7%;  Pred. No. 61;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 gtggagcctcaacatcctg 21
          |||||||||||||||| ||
Db   1315 gtggagcctcaacatcttg 1333


RESULT  10
AAC57733
ID   AAC57733 standard; DNA; 1001 BP.
XX
AC   AAC57733;
XX
DT   25-JAN-2001  (first entry)
XX
DE   Arachidonic acid metabolism related genomic biallelic marker #367.
XX
KW   Human; biallelic marker; arachidonic acid metabolism; genotyping;
KW   detection; hybridisation; phenotype; haplotype; SNP; polymorphic base;
KW   single nucleotide polymorphism; hybridisation assay; sequencing assay;
KW   specific amplification assay; identification; ERBM; 12-LO-RBM;
KW   eicosanoid-related biallelic marker; 12-LO-related biallelic marker; ds.
XX
OS   Homo sapiens.
XX
PN   WO200047771-A2.
XX
PD   17-AUG-2000.
XX
PF   11-FEB-2000; 2000WO-IB00184.
XX
PR   12-FEB-1999;   99US-0119917.
PR   23-MAR-1999;   99US-0275267.
PR   07-MAY-1999;   99US-0133200.
XX
PA   (GEST ) GENSET.
XX
PI   Blumenfeld M,  Bougueleret L,  Chumakov I;
XX
DR   WPI; 2000-571881/53.
XX
PT   Novel biallelic markers useful for detecting conditions and genotypes
PT   associated with arachidonic acid metabolism -
XX
PS   Claim 13; Page 543; 802pp; English.
XX
CC   The present invention describes polynucleotides including biallelic
CC   markers derived from genes involved in arachidonic acid metabolism and
CC   from genomic regions flanking those genes. Methods from the present
CC   invention may be used to select individuals for clinical trials and
CC   predict responses to treatment with drugs. The polynucleotides may be
CC   used in hybridisation assays, sequencing assays and specific
CC   amplification assays for identifying an eicosanoid-related biallelic
CC   marker (ERBM) or 12-LO-related biallelic marker, and for amplifying a
CC   segment of nucleotides containing an ERBM. The polynucleotides are
CC   useful in diagnostic kits. The markers may be used to detect conditions
CC   and genotypes associated with arachidonic acid metabolism. AAC57367 to
CC   AAC58018 and AAB24019 and AAB24020 represent sequences used in the
CC   exemplification of the present invention.
CC   N.B. Polymorphic bases (single nucleotide polymorphisms also known as
CC   SNPs) in the polynucleotide sequences from the present invention have
CC   been given as their corresponding degenerate bases e.g. a polymorphic
CC   base of C or T has been given as Y.
XX
SQ   Sequence 1001 BP; 304 A; 177 C; 195 G; 324 T; 1 other;


  Query Match             80.0%;  Score 16.8;  DB 21;  Length 1001;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 gtgtggagcctcaacatcct 20
          |||||||||  || |||||||
Db    444 gtgtggagcttccacatcct 463


RESULT  11
AAC57734
ID   AAC57734 standard; DNA; 1001 BP.
XX
AC   AAC57734;
XX
DT   25-JAN-2001  (first entry)
XX
DE   Arachidonic acid metabolism related genomic biallelic marker #368.
XX
KW   Human; biallelic marker; arachidonic acid metabolism; genotyping;
KW   detection; hybridisation; phenotype; haplotype; SNP; polymorphic base;
KW   single nucleotide polymorphism; hybridisation assay; sequencing assay;
KW   specific amplification assay; identification; ERBM; 12-LO-RBM;
KW   eicosanoid-related biallelic marker; 12-LO-related biallelic marker; ds.
XX
OS   Homo sapiens.
XX
PN   WO200047771-A2.
XX
PD   17-AUG-2000.
XX
PF   11-FEB-2000; 2000WO-IB00184.
XX
PR   12-FEB-1999;   99US-0119917.
PR   23-MAR-1999;   99US-0275267.
PR   07-MAY-1999;   99US-0133200.
XX
PA   (GEST ) GENSET.
XX
PI   Blumenfeld M,  Bougueleret L,  Chumakov I;
XX
DR   WPI; 2000-571881/53.
XX
PT   Novel biallelic markers useful for detecting conditions and genotypes
PT   associated with arachidonic acid metabolism -
XX
PS   Claim 13; Page 544; 802pp; English.
XX
CC   The present invention describes polynucleotides including biallelic
CC   markers derived from genes involved in arachidonic acid metabolism and
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CC   from genomic regions flanking those genes. Methods from the present
CC   invention may be used to select individuals for clinical trials and
CC   predict responses to treatment with drugs. The polynucleotides may be
CC   used in hybridisation assays, sequencing assays and specific
CC   amplification assays for identifying an eicosanoid-related biallelic
CC   marker (ERBM) or 12-LO-related biallelic marker, and for amplifying a
CC   segment of nucleotides containing an ERBM. The polynucleotides are
CC   useful in diagnostic kits. The markers may be used to detect conditions
CC   and genotypes associated with arachidonic acid metabolism. AAC57367 to
CC   AAC58018 and AAB24019 and AAB24020 represent sequences used in the
CC   exemplification of the present invention.
CC   N.B. Polymorphic bases (single nucleotide polymorphisms also known as
CC   SNPs) in the polynucleotide sequences from the present invention have
CC   been given as their corresponding degenerate bases e.g. a polymorphic
CC   base of C or T has been given as Y.
XX
SQ   Sequence 1001 BP; 308 A; 183 C; 202 G; 307 T; 1 other;


  Query Match             80.0%;  Score 16.8;  DB 21;  Length 1001;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 gtgtggagcctcaacatcct 20
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RESULT  12
ABA15833/c
ID   ABA15833 standard; DNA; 32249 BP.
XX
AC   ABA15833;
XX
DT   23-JAN-2002  (first entry)
XX
DE   Human nervous system related polynucleotide SEQ ID NO 8164.
XX
KW   Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW   immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW   antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
KW   antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW   antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
KW   antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW   neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS   Homo sapiens.
XX
PN   WO200159063-A2.
XX
PD   16-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01334.
XX
PR   31-JAN-2000; 2000US-0179065.
PR   04-FEB-2000; 2000US-0180628.
PR   24-FEB-2000; 2000US-0184664.
PR   02-MAR-2000; 2000US-0186350.
PR   16-MAR-2000; 2000US-0189874.
PR   17-MAR-2000; 2000US-0190076.
PR   18-APR-2000; 2000US-0198123.
PR   19-MAY-2000; 2000US-0205515.
PR   07-JUN-2000; 2000US-0209467.
PR   28-JUN-2000; 2000US-0214886.
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PR   07-JUL-2000; 2000US-0216647.
PR   07-JUL-2000; 2000US-0216880.
PR   11-JUL-2000; 2000US-0217487.
PR   11-JUL-2000; 2000US-0217496.
PR   14-JUL-2000; 2000US-0218290.
PR   26-JUL-2000; 2000US-0220963.
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PR   14-AUG-2000; 2000US-0225213.
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PR   14-AUG-2000; 2000US-0225266.
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PR   14-AUG-2000; 2000US-0225447.
PR   14-AUG-2000; 2000US-0225757.
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PR   18-AUG-2000; 2000US-0226279.
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PR   22-AUG-2000; 2000US-0227182.
PR   23-AUG-2000; 2000US-0227009.
PR   30-AUG-2000; 2000US-0228924.
PR   01-SEP-2000; 2000US-0229287.
PR   01-SEP-2000; 2000US-0229343.
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PR   05-SEP-2000; 2000US-0229509.
PR   05-SEP-2000; 2000US-0229513.
PR   06-SEP-2000; 2000US-0230437.
PR   06-SEP-2000; 2000US-0230438.
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PR   12-SEP-2000; 2000US-0231968.
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PR   14-SEP-2000; 2000US-0232400.
PR   14-SEP-2000; 2000US-0232401.
PR   14-SEP-2000; 2000US-0233063.
PR   14-SEP-2000; 2000US-0233064.
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PR   21-SEP-2000; 2000US-0234223.
PR   21-SEP-2000; 2000US-0234274.
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PR   26-SEP-2000; 2000US-0235484.
PR   27-SEP-2000; 2000US-0235834.
PR   27-SEP-2000; 2000US-0235836.
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PR   29-SEP-2000; 2000US-0236368.
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PR   29-SEP-2000; 2000US-0236370.
PR   02-OCT-2000; 2000US-0236802.
PR   02-OCT-2000; 2000US-0237037.
PR   02-OCT-2000; 2000US-0237038.
PR   02-OCT-2000; 2000US-0237039.
PR   02-OCT-2000; 2000US-0237040.
PR   13-OCT-2000; 2000US-0239935.
PR   13-OCT-2000; 2000US-0239937.
PR   20-OCT-2000; 2000US-0240960.
PR   20-OCT-2000; 2000US-0241785.
PR   20-OCT-2000; 2000US-0241786.
PR   20-OCT-2000; 2000US-0241787.
PR   20-OCT-2000; 2000US-0241808.
PR   20-OCT-2000; 2000US-0241809.
PR   20-OCT-2000; 2000US-0241826.
PR   20-OCT-2000; 2000US-0242221.
PR   01-NOV-2000; 2000US-0244617.
PR   08-NOV-2000; 2000US-0246474.
PR   08-NOV-2000; 2000US-0246475.
PR   08-NOV-2000; 2000US-0246476.
PR   08-NOV-2000; 2000US-0246477.
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PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
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PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
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PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-541565/60.
XX
PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
PT cancers and metastases -
XX
PS Disclosure; SEQ ID NO 8164; 1701pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 32249 BP; 9422 A; 6351 C; 6314 G; 10162 T; 0 other;

Query Match 80.0%; Score 16.8; DB 22; Length 32249;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 tgtggagcctcaacatcctg 21
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Db 22426 TGTGCAGCCTCAACCTCCTG 22407

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AC AAL03071;
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DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 5759.
XX
KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200155320-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01339.
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PR 02-OCT-2000; 2000US-0236802.
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PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
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PR 01-DEC-2000; 2000US-0250160.
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PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465570/50.
XX
PT Isolated nucleic acid molecule encoding a reproductive system antigen
PT is used in preventing, treating or ameliorating a medical condition -
XX
PS Disclosure; SEQ ID NO 5759; 1297pp + Sequence Listing; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention.
XX
SQ Sequence 32249 BP; 9422 A; 6351 C; 6314 G; 10162 T; 0 other;

Query Match 80.0%; Score 16.8; DB 22; Length 32249;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 tgtggagcctcaacatcctg 21
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Db 22426 TGTGCAGCCTCAACCTCCTG 22407

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XX
AC AAC29479;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 33554.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX

PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS Claim 1; SEQ ID 33554; 71pp + CD-ROM; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.
XX
SQ Sequence 211 BP; 48 A; 45 C; 46 G; 71 T; 1 other;

Query Match 78.1%; Score 16.4; DB 21; Length 211;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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XX
AC AAC25147;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 29222.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS Claim 1; SEQ ID 29222; 71pp + CD-ROM; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.
XX
SQ Sequence 246 BP; 50 A; 69 C; 38 G; 89 T; 0 other;

Query Match 78.1%; Score 16.4; DB 21; Length 246;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 25	14.8	70.5	24	1	US-08-219-633-1	Sequence 1, Appli
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38	14.8	70.5	1018	1	US-08-443-130-6	Sequence 6, Appli
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ALIGNMENTS

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; Patent No. 6355425
; GENERAL INFORMATION:
;  APPLICANT: Rothenberg, Barry E.
;  APPLICANT:  Sawada-Hirai, Ritsuko
;  APPLICANT:  Barton, James C.
;  TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
;  FILE REFERENCE: 10653/002001
;  CURRENT APPLICATION NUMBER: US/09/277,457
;  CURRENT FILING DATE:  1999-03-26
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-09-277-457-15


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RESULT 2
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; Sequence 1, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
```

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;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94111-3834
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/652,265
;       FILING DATE:  23-MAY-1996
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith, William M.
;       REGISTRATION NUMBER:  30,223
;       REFERENCE/DOCKET NUMBER:  17957-000500
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 576-0200
;       TELEFAX:  (415) 576-0300
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10825 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;       LOCATION:  6040..6153, 7107..7147)
;       OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;       OTHER INFORMATION:
;       OTHER INFORMATION:  /note= "No. 6025130mal or wild-type (unaffected)
;       OTHER INFORMATION:  Hereditary Hemochromatosis (HH) gene
;       OTHER INFORMATION:  allele"
;     FEATURE:
;       NAME/KEY:  -
;       LOCATION:  140..7319
;       OTHER INFORMATION:  /note= "start and stop positions for
;       OTHER INFORMATION:  normal or wild-type (unaffected) allele
;       OTHER INFORMATION:  cDNA (SEQ ID NO:9)"
;     FEATURE:
;       NAME/KEY:  -
;       LOCATION:  3852..3891
;       OTHER INFORMATION:  /note= "start and stop positions for
;       OTHER INFORMATION:  normal or wild-type (unaffected) genomic
;       OTHER INFORMATION:  sequence surrounding variant for 24d2(C)
;       OTHER INFORMATION:  allele (SEQ ID NO:41)"
;     FEATURE:
;       NAME/KEY:  -
;       LOCATION:  5507..6023
;       OTHER INFORMATION:  /note= "start and stop positions for
;       OTHER INFORMATION:  normal or wild-type (unaffected) genomic
;       OTHER INFORMATION:  sequence surrounding variant for 24d1(G)
;       OTHER INFORMATION:  allele (SEQ ID NO:20)"
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(3872, "c")
;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d2
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(3878, "a")
;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d7
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(5834, "g")
;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d1
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US-08-652-265-1


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  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtgtggagcctcaacatcctg 21
          |||||||||||||||||||||
Db   3695 GTGTGGAGCCTCAACATCCTG 3715


RESULT   3
US-08-652-265-3
; Sequence 3, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  mutation"
;      OTHER INFORMATION:  /note= "Hereditary Hemochromatosis (HH)
;      OTHER INFORMATION:  gene 24d1 allele"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  24d1 allele cDNA (SEQ ID NO:10)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  3852..3891
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;       OTHER INFORMATION:  /note= "start and stop positions for
;       OTHER INFORMATION:  genomic sequence surrounding variant
;       OTHER INFORMATION:  for 24d2(C) allele (SEQ ID NO:41)"
;     FEATURE:
;       NAME/KEY:  -
;       LOCATION:  5507..6023
;       OTHER INFORMATION:  /note= "start and stop positions for
;       OTHER INFORMATION:  genomic sequence surrounding variant
;       OTHER INFORMATION:  for 24d1(A) allele (SEQ ID NO:21)"
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(5834, "a")
;       OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;       OTHER INFORMATION:
;       OTHER INFORMATION:  /label= 24d1
US-08-652-265-3


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Db    3695 GTGTGGAGCCTCAACATCCTG 3715


RESULT   4
US-08-652-265-5
; Sequence 5, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  mutation"
;      OTHER INFORMATION:  /note= "Hereditary Hemochromatosis (HH)
;      OTHER INFORMATION:  gene 24d2 allele"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  24d2 allele cDNA (SEQ ID NO:11)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  3852..3891
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d2(G) allele (SEQ ID NO:42)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  5507..6023
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d1(G) allele (SEQ ID NO:20)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(3872, "g")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d2
US-08-652-265-5


  Query Match           100.0%;  Score 21;  DB 3;  Length 10825;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 gtgtggagcctcaacatcctg 21
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Db    3695 GTGTGGAGCCTCAACATCCTG 3715


RESULT   5
US-08-652-265-7
; Sequence 7, Application US/08652265
; Patent No. 6025130
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
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;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  17957-000500
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  and 24d2 mutations"
;      OTHER INFORMATION:  /note= "Hereditary Hemochromatosis (HH)
;      OTHER INFORMATION:  gene containing a combination of both
;      OTHER INFORMATION:  24d1 and 24d2 alleles"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  cDNA containing a combination of both
;      OTHER INFORMATION:  24d1 and 24d2 alleles
;      OTHER INFORMATION:  (SEQ ID NO:12)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  3852..3891
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d2(G) allele (SEQ ID NO:42)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  5507..6023
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d1(A) allele (SEQ ID NO:21)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(3872, "g")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d2
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;      NAME/KEY:  allele
;      LOCATION:  replace(5834, "a")
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;      OTHER INFORMATION:
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US-08-652-265-7


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Db    3695 GTGTGGAGCCTCAACATCCTG 3715


RESULT   6
US-08-834-497A-1
; Sequence 1, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /note= "No. 6140305mal or wild-type (unaffected)
;      OTHER INFORMATION:  Hereditary Hemochromatosis (HH) gene
;      OTHER INFORMATION:  allele"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  normal or wild-type (unaffected) allele
;      OTHER INFORMATION:  cDNA (SEQ ID NO:9)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  3852..3891
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  normal or wild-type (unaffected) genomic
;      OTHER INFORMATION:  sequence surrounding variant for 24d2(C)
;      OTHER INFORMATION:  allele (SEQ ID NO:41)"
;    FEATURE:
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;       NAME/KEY:  -
;       LOCATION:  5507..6023
;       OTHER INFORMATION:  /note= "start and stop positions for
;       OTHER INFORMATION:  normal or wild-type (unaffected) genomic
;       OTHER INFORMATION:  sequence surrounding variant for 24d1(G)
;       OTHER INFORMATION:  allele (SEQ ID NO:20)"
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(3872, "c")
;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d2
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;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
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;       NAME/KEY:  allele
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;       OTHER INFORMATION:  /phenotype= "normal or wild-type
;       OTHER INFORMATION:  (unaffected)"
;       OTHER INFORMATION:  /label= 24d1
US-08-834-497A-1


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  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db   3695 GTGTGGAGCCTCAACATCCTG 3715


RESULT   7
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; Sequence 3, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  mutation"
;      OTHER INFORMATION:  /note= "Hereditary Hemochromatosis (HH)
;      OTHER INFORMATION:  gene 24d1 allele"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  24d1 allele cDNA (SEQ ID NO:10)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  3852..3891
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d2(C) allele (SEQ ID NO:41)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  5507..6023
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d1(A) allele (SEQ ID NO:21)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(5834, "a")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d1
US-08-834-497A-3


  Query Match             100.0%;  Score 21;  DB 3;  Length 10825;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtgtggagcctcaacatcctg 21
          |||||||||||||||||||||
Db   3695 GTGTGGAGCCTCAACATCCTG 3715


RESULT   8
US-08-834-497A-5
; Sequence 5, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
```

```
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  mutation"
;      OTHER INFORMATION:  /note= "Hereditary Hemochromatosis (HH)
;      OTHER INFORMATION:  gene 24d2 allele"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  24d2 allele cDNA (SEQ ID NO:11)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  3852..3891
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d2(G) allele (SEQ ID NO:42)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  5507..6023
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d1(G) allele (SEQ ID NO:20)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(3872, "g")
;      OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /label= 24d2
US-08-834-497A-5


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Qy       1 gtgtggagcctcaacatcctg 21
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Db    3695 GTGTGGAGCCTCAACATCCTG 3715


RESULT   9
US-08-834-497A-7
; Sequence 7, Application US/08834497A
; Patent No. 6140305
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
;    NUMBER OF SEQUENCES:  76
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,497A
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/652,265
;      FILING DATE:  23-MAY-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/632,673
;      FILING DATE:  16-APR-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,912
;      FILING DATE:  04-APR-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0056-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
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;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;       LOCATION:  6040..6153, 7107..7147)
;       OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;       OTHER INFORMATION:
;       OTHER INFORMATION:  and 24d2 mutations"
;       OTHER INFORMATION:  /note= "Hereditary Hemochromatosis (HH)
;       OTHER INFORMATION:  gene containing a combination of both
;       OTHER INFORMATION:  24d1 and 24d2 alleles"
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;       NAME/KEY:  -
;       LOCATION:  140..7319
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;       OTHER INFORMATION:  24d1 and 24d2 alleles
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;     FEATURE:
;       NAME/KEY:  -
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;       OTHER INFORMATION:  genomic sequence surrounding variant
;       OTHER INFORMATION:  for 24d2(G) allele (SEQ ID NO:42)"
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;       LOCATION:  5507..6023
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;       LOCATION:  replace(3872, "g")
;       OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;       OTHER INFORMATION:
;       OTHER INFORMATION:  /label= 24d2
;     FEATURE:
;       NAME/KEY:  allele
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;       OTHER INFORMATION:
;       OTHER INFORMATION:  /label= 24d1
US-08-834-497A-7


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Db   3695 GTGTGGAGCCTCAACATCCTG 3715


RESULT  10
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; Sequence 1, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  /note= "No. 6228594mal or wild-type (unaffected)
;      OTHER INFORMATION:  Hereditary Hemochromatosis (HH) gene
;      OTHER INFORMATION:  allele"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  normal or wild-type (unaffected) allele
;      OTHER INFORMATION:  cDNA (SEQ ID NO:9)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  3852..3891
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;      OTHER INFORMATION:  normal or wild-type (unaffected) genomic
;      OTHER INFORMATION:  sequence surrounding variant for 24d2(C)
;      OTHER INFORMATION:  allele (SEQ ID NO:41)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  5507..6023
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;      OTHER INFORMATION:  normal or wild-type (unaffected) genomic
;      OTHER INFORMATION:  sequence surrounding variant for 24d1(G)
;      OTHER INFORMATION:  allele (SEQ ID NO:20)"
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;      NAME/KEY:  allele
;      LOCATION:  replace(3872, "c")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
;      OTHER INFORMATION:  /label= 24d2
;    FEATURE:
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;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(5834, "g")
;      OTHER INFORMATION:  /phenotype= "normal or wild-type
;      OTHER INFORMATION:  (unaffected)"
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US-09-503-444A-1


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Qy      1 gtgtggagcctcaacatcctg 21
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Db   3695 GTGTGGAGCCTCAACATCCTG 3715


RESULT  11
US-09-503-444A-3
; Sequence 3, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  mutation"
;      OTHER INFORMATION:  /note= "Hereditary Hemochromatosis (HH)
;      OTHER INFORMATION:  gene 24d1 allele"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  24d1 allele cDNA (SEQ ID NO:10)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  3852..3891
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d2(C) allele (SEQ ID NO:41)"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  5507..6023
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  genomic sequence surrounding variant
;      OTHER INFORMATION:  for 24d1(A) allele (SEQ ID NO:21)"
;    FEATURE:
;      NAME/KEY:  allele
;      LOCATION:  replace(5834, "a")
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US-09-503-444A-3


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Db   3695 GTGTGGAGCCTCAACATCCTG 3715


RESULT  12
US-09-503-444A-5
; Sequence 5, Application US/09503444A
; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
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;       SOFTWARE:  WordPerfect Version 8
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/503,444A
;       FILING DATE:  14-Feb-2000
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/652,265
;       FILING DATE:  23-May-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/632,673
;       FILING DATE:  16-Apr-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/630,912
;       FILING DATE:  04-Apr-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Poissant, Brian M.
;       REGISTRATION NUMBER:  28,462
;       REFERENCE/DOCKET NUMBER:  8907-0088-999
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  212-790-9090
;       TELEFAX:  212-869-9741
;       TELEX:  66141
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10825 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;       LOCATION:  6040..6153, 7107..7147)
;       OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;       OTHER INFORMATION:
;       OTHER INFORMATION:  mutation"
;       OTHER INFORMATION:  /note= "Hereditary Hemochromatosis (HH)
;       OTHER INFORMATION:  gene 24d2 allele"
;     FEATURE:
;       NAME/KEY:  -
;       LOCATION:  140..7319
;       OTHER INFORMATION:  /note= "start and stop positions for
;       OTHER INFORMATION:  24d2 allele cDNA (SEQ ID NO:11)"
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;       NAME/KEY:  -
;       LOCATION:  3852..3891
;       OTHER INFORMATION:  /note= "start and stop positions for
;       OTHER INFORMATION:  genomic sequence surrounding variant
;       OTHER INFORMATION:  for 24d2(G) allele (SEQ ID NO:42)"
;     FEATURE:
;       NAME/KEY:  -
;       LOCATION:  5507..6023
;       OTHER INFORMATION:  /note= "start and stop positions for
;       OTHER INFORMATION:  genomic sequence surrounding variant
;       OTHER INFORMATION:  for 24d1(G) allele (SEQ ID NO:20)"
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(3872, "g")
;       OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
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;       OTHER INFORMATION:  /label= 24d2
US-09-503-444A-5


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Qy       1 gtgtggagcctcaacatcctg 21
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Db    3695 GTGTGGAGCCTCAACATCCTG 3715
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; Patent No. 6228594
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Winston J.
;    APPLICANT:  Drayna, Dennis T.
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Gnirke, Andreas
;    APPLICANT:  Ruddy, David
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Hereditary Hemochromatosis Gene
;    NUMBER OF SEQUENCES:  44
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect Version 8
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/503,444A
;      FILING DATE:  14-Feb-2000
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/652,265
;      FILING DATE:  23-May-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,673
;      FILING DATE:  16-Apr-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/630,912
;      FILING DATE:  04-Apr-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Poissant, Brian M.
;      REGISTRATION NUMBER:  28,462
;      REFERENCE/DOCKET NUMBER:  8907-0088-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10825 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(361..436, 3762..4025, 4235..4510, 5606..5881,
;      LOCATION:  6040..6153, 7107..7147)
;      OTHER INFORMATION:  /product= "Hereditary Hemochromatosis
;      OTHER INFORMATION:
;      OTHER INFORMATION:  and 24d2 mutations"
;      OTHER INFORMATION:  /note= "Hereditary Hemochromatosis (HH)
;      OTHER INFORMATION:  gene containing a combination of both
;      OTHER INFORMATION:  24d1 and 24d2 alleles"
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  140..7319
;      OTHER INFORMATION:  /note= "start and stop positions for
;      OTHER INFORMATION:  cDNA containing a combination of both
;      OTHER INFORMATION:  24d1 and 24d2 alleles
;      OTHER INFORMATION:  (SEQ ID NO:12)"
;    FEATURE:
;      NAME/KEY:  -
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;       LOCATION:  3852..3891
;       OTHER INFORMATION:  /note= "start and stop positions for
;       OTHER INFORMATION:  genomic sequence surrounding variant
;       OTHER INFORMATION:  for 24d2(G) allele (SEQ ID NO:42)"
;     FEATURE:
;       NAME/KEY:  -
;       LOCATION:  5507..6023
;       OTHER INFORMATION:  /note= "start and stop positions for
;       OTHER INFORMATION:  genomic sequence surrounding variant
;       OTHER INFORMATION:  for 24d1(A) allele (SEQ ID NO:21)"
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(3872, "g")
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;       OTHER INFORMATION:
;       OTHER INFORMATION:  /label= 24d2
;     FEATURE:
;       NAME/KEY:  allele
;       LOCATION:  replace(5834, "a")
;       OTHER INFORMATION:  /phenotype= "Hereditary Hemochromatosis
;       OTHER INFORMATION:
;       OTHER INFORMATION:  /label= 24d1
US-09-503-444A-7


  Query Match             100.0%;  Score 21;  DB 4;  Length 10825;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtgtggagcctcaacatcctg 21
          |||||||||||||||||||||
Db   3695 GTGTGGAGCCTCAACATCCTG 3715


RESULT  14
US-09-277-457-27
; Sequence 27, Application US/09277457
; Patent No. 6355425
; GENERAL INFORMATION:
;  APPLICANT: Rothenberg, Barry E.
;  APPLICANT:  Sawada-Hirai, Ritsuko
;  APPLICANT:  Barton, James C.
;  TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
;  FILE REFERENCE: 10653/002001
;  CURRENT APPLICATION NUMBER: US/09/277,457
;  CURRENT FILING DATE:  1999-03-26
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
;   LENGTH: 12146
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-09-277-457-27


  Query Match             100.0%;  Score 21;  DB 4;  Length 12146;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtgtggagcctcaacatcctg 21
          |||||||||||||||||||||
Db   4585 gtgtggagcctcaacatcctg 4605


RESULT  15
US-08-724-394A-20
; Sequence 20, Application US/08724394A
; Patent No. 5872237
;  GENERAL INFORMATION:
;    APPLICANT:  Feder, John N.
;    APPLICANT:  Kronmal, Gregory S.
;    APPLICANT:  Lauer, Peter M.
;    APPLICANT:  Ruddy, David A.
;    APPLICANT:  Thomas, Winston
;    APPLICANT:  Tsuchihashi, Zenta
;    APPLICANT:  Wolff, Roger K.
;    TITLE OF INVENTION:  Megabase Transcript Map:  No. 5872237el
;    TITLE OF INVENTION:  Sequences and Antibodies Thereto
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/724,394A
;      FILING DATE:  01-OCT-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitts, Renee A.
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  017957-000100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-576-0200
;      TELEFAX:  415-576-0300
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  246240 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..246240
;      OTHER INFORMATION:  /note= "HLA-H.CONTIG"
US-08-724-394A-20


  Query Match             100.0%;  Score 21;  DB 2;  Length 246240;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gtgtggagcctcaacatcctg 21
          |||||||||||||||||||||
Db 195998 GTGTGGAGCCTCAACATCCTG 196018


Search completed: July 16, 2002, 09:53:36
Job time: 8829 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 07:17:27 ; Search time 1777.36 Seconds
(without alignments)
159.470 Million cell updates/sec

Title: US-09-981-606-15
Perfect score: 21
Sequence: 1 gtgtggagcctcaacatcctg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	18	85.7	494	12	AQ253896	AQ253896 HS_3245_B
	2	17.8	84.8	474	9	AW664669	AW664669 hi84d02.x
c	3	17.8	84.8	507	10	BF354879	BF354879 RC1-HT079
c	4	17.8	84.8	583	10	BM177573	BM177573 saj63a05.
c	5	17.4	82.9	382	12	FR0004308	Z88091 F.rubripes
	6	17.4	82.9	393	12	AQ605972	AQ605972 HS_5383_A
	7	17.4	82.9	427	12	FR0004279	Z88062 F.rubripes
c	8	17.4	82.9	534	9	AA851662	AA851662 EST194430
c	9	17.4	82.9	619	12	FR0004290	Z88073 F.rubripes
c	10	17.4	82.9	619	12	FR0004298	Z88081 F.rubripes
c	11	17.4	82.9	619	12	FR0004319	Z88102 F.rubripes
	12	17.4	82.9	651	10	BE876167	BE876167 601485668
c	13	16.8	80.0	229	10	BM029637	BM029637 IpSkn0215
c	14	16.8	80.0	291	9	BB413927	BB413927 BB413927
	15	16.8	80.0	297	9	AA483942	AA483942 ne92e08.s
	16	16.8	80.0	313	10	BF042964	BF042964 BP250009B
	17	16.8	80.0	320	10	T98950	T98950 ye66h02.s1
c	18	16.8	80.0	327	10	BF417623	BF417623 UI-R-CN0-
	19	16.8	80.0	398	12	AZ292926	AZ292926 RPCI-23-1
c	20	16.8	80.0	419	9	AI887031	AI887031 wl95f07.x
c	21	16.8	80.0	427	9	AA935116	AA935116 op46g08.s
c	22	16.8	80.0	451	9	AI225116	AI225116 qi32g09.x
c	23	16.8	80.0	461	12	AQ705494	AQ705494 HS_5526_B
	24	16.8	80.0	468	9	AL580728	AL580728 AL580728
	25	16.8	80.0	489	9	AI552933	AI552933 vg58e03.y
	26	16.8	80.0	513	12	AQ281158	AQ281158 RPCI11-92
	27	16.8	80.0	545	10	BF198466	BF198466 248401 MA
c	28	16.8	80.0	560	12	AQ267259	AQ267259 RPCI11-68
	29	16.8	80.0	613	10	BJ005580	BJ005580 BJ005580
c	30	16.8	80.0	686	12	BH272225	BH272225 CH230-23G
	31	16.8	80.0	790	12	BH373312	BH373312 AG-ND-152
	32	16.8	80.0	824	12	CNS01PKZ	AL154947 Anopheles
c	33	16.8	80.0	871	12	CNS01FV9	AL142342 Anopheles
	34	16.4	78.1	208	10	T63515	T63515 yc07a02.s1
	35	16.4	78.1	243	10	BF928299	BF928299 IL2-NT020
	36	16.4	78.1	284	9	BB844837	BB844837 BB844837
c	37	16.4	78.1	284	9	AA491790	AA491790 ne96g03.s
c	38	16.4	78.1	288	10	BG977497	BG977497 RC5-CI016
	39	16.4	78.1	288	10	H75692	H75692 yr77h07.r1
c	40	16.4	78.1	318	9	AA285249	AA285249 PMY0752 K
	41	16.4	78.1	336	9	AA657483	AA657483 nt66e01.s
	42	16.4	78.1	357	9	AW265167	AW265167 xp80g10.x
	43	16.4	78.1	358	12	AQ071213	AQ071213 HS_2174_A
	44	16.4	78.1	368	9	AA652101	AA652101 ns50d08.s
c	45	16.4	78.1	369	10	H92176	H92176 ys87b05.s1

ALIGNMENTS

RESULT 1
AQ253896/c
LOCUS AQ253896 494 bp DNA linear GSS 10-OCT-1998
DEFINITION HS_3245_B2_G03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=6 Row=N, DNA sequence.
ACCESSION AQ253896
VERSION AQ253896.1 GI:3725250
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 494)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3245 row: N column: 6
Class: BAC ends
High quality sequence stop: 494.
FEATURES Location/Qualifiers
source 1. .494
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3245 Col=6 Row=N"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

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BASE COUNT      142 a    111 c     90 g    147 t      4 others
ORIGIN


  Query Match             85.7%;  Score 18;  DB 12;  Length 494;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 tggagcctcaacatcctg 21
          ||||||||||||||||||
Db    150 TGGAGCCTCAACATCCTG 133


RESULT   2
AW664669
LOCUS       AW664669                 474 bp    mRNA    linear   EST 06-APR-2000
DEFINITION  hi84d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:2978979 3', mRNA sequence.
ACCESSION   AW664669
VERSION     AW664669.1  GI:7457212
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 474)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40UP from Gibco
            High quality sequence stop: 473.
FEATURES             Location/Qualifiers
     source          1. .474
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2978979"
                     /clone_lib="Soares_NFL_T_GBC_S1"
                     /lab_host="DH10B"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from three normalized
                     libraries (fetal lung NbHL19W, testis NHT, and B-cell
                     NCI_CGAP_GCB1) were mixed, and ss circles were made in
                     vitro. Following HAP purification, this DNA was used as
                     tracer in a subtractive hybridization reaction. The driver
                     was PCR-amplified cDNAs from pools of 5,000 clones made
                     from the same 3 libraries. The pools consisted of
                     I.M.A.G.E. clones 297480-302087, 682632-687239,
                     726408-728711, and 729096-731399. Subtraction by Bento
                     Soares and M. Fatima Bonaldo.  "
BASE COUNT      131 a    103 c    107 g    133 t
ORIGIN


  Query Match             84.8%;  Score 17.8;  DB 9;  Length 474;
  Best Local Similarity   90.5%;  Pred. No. 5e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 gtgtggagcctcaacatcctg 21
          ||| |||| ||||||||||||
Db    361 GTGAGGAGGCTCAACATCCTG 381


RESULT   3
BF354879/c
LOCUS       BF354879                 507 bp    mRNA    linear   EST 22-NOV-2000
DEFINITION  RC1-HT0797-210600-011-g12 HT0797 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF354879
VERSION     BF354879.1  GI:11313953
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 507)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-HT0797-
            210600-011-g12&t3=2000-06-21&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 9
            High quality sequence stop: 507.
FEATURES             Location/Qualifiers
     source          1. .507
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="HT0797"
                     /dev_stage="Adult"
                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT      166 a    101 c     92 g    148 t
ORIGIN


  Query Match             84.8%;  Score 17.8;  DB 10;  Length 507;
  Best Local Similarity   90.5%;  Pred. No. 5.1e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 gtgtggagcctcaacatcctg 21
          ||||| ||| ||||||||||||
Db     55 GTGTGAAGCTTCAACATCCTG 35


RESULT   4
BM177573/c
LOCUS       BM177573                 583 bp    mRNA    linear   EST 06-DEC-2001
DEFINITION  saj63a05.y1 Gm-c1072 Glycine max cDNA clone SOYBEAN CLONE ID:
            Gm-c1072-4234 5' similar to TR:Q9SHY5 Q9SHY5 F1E22.7. ;, mRNA
            sequence.
ACCESSION   BM177573
VERSION     BM177573.1  GI:17400791
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
```

```
REFERENCE   1  (bases 1 to 583)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: ResGen, Invitrogen Corp. 2130
            South Memorial Parkway Huntsville, AL 35801 For further information
            call: (800)-533-4363 or contact: ccu@resgen.com web site:
            www.resgen.com
            Seq primer: -40RP from Gibco
            High quality sequence stop: 444.
FEATURES             Location/Qualifiers
     source          1. .583
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /clone="SOYBEAN CLONE ID: Gm-c1072-4234"
                     /clone_lib="Gm-c1072"
                     /tissue_type="seedlings induced for symptoms of SDS
                     (Sudden Death Syndrome) disease"
                     /dev_stage="2-3 weeks old"
                     /lab_host="DH10B"
                     /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                     XhoI; The cDNA library wms constructed from mRNA isolated
                     from 2-3 week old seedlings that were induced for symptoms
                     of SDS (Sudden Death Syndrome) disease by the
                     translocation of culture filtrate of Fusarium solani f.
                     sp. glycines (Plant Cell Report 18:375-380). Cultivar PI
                     567374 is partially resistant to the disease SDS. Plant
                     tissue (expanded leaves, folded leaves, and new shoots)
                     were collected at 1, 6, 24, and 48 hrs. after inoculation
                     and their mRNA pooled equally for cDNA construction. The
                     library was prepared using the Stratagene pBluescript II
                     SK(+) library construction kit. Complementary DNA was
                     synthesized from mRNA using a primer consisting of a
                     poly(dT) sequence with an XhoI restriction site. EcoRI
                     adaptors were ligated to the blunt-ended cDNA fragments
                     followed by XhoI digestion. The cDNA insert is protected
                     from XhoI digestion via methylation during first strand
                     synthesis. The cDNA fragments were directionally cloned
                     into the EcoRI-XhoI restriction site of the pBluescript
                     vector. The ligated cDNA fragments were transformed into
                     E.coli ElectroMax DH10B host cells. Plants were inoculated
                     by Shuxian Li (Glen Hartman lab, University of Illinois).
                     Library was constructed by Steve Clough (Lila Vodkin lab,
                     University of Illinois)."
BASE COUNT      181 a    130 c    127 g    145 t
ORIGIN


  Query Match             84.8%;  Score 17.8;  DB 10;  Length 583;
  Best Local Similarity   90.5%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 gtgtggagcctcaacatcctg 21
           |||||| |||||||||| ||
Db      79 GTGTGGTGCCTCAACATCATG 59


RESULT   5
FR0004308/c
LOCUS       FR0004308               382 bp    DNA     linear   GSS 27-FEB-1997
DEFINITION  F.rubripes GSS sequence, clone 045H22aF10, genomic survey sequence.

ACCESSION   Z88091
VERSION     Z88091.1  GI:1885003
KEYWORDS    GSS; genome survey sequence.
SOURCE      Takifugu rubripes.
  ORGANISM  Takifugu rubripes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Takifugu.
REFERENCE   1  (bases 1 to 382)
  AUTHORS   Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
            Williams,G. and Brenner,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource
            Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
COMMENT     Vector: m13mp18
            V_type: phage
            PRIMER: M13
            DESCR:
            One pass dye-terminator sequencing of cosmid cloned genomic
            sequence.
FEATURES             Location/Qualifiers
     source          1. .382
                     /organism="Takifugu rubripes"
                     /db_xref="taxon:31033"
                     /clone_lib="cosmid 045H22"
                     /clone="045H22aF10"
BASE COUNT      105 a     93 c     86 g     95 t      3 others
ORIGIN


  Query Match             82.9%;  Score 17.4;  DB 12;  Length 382;
  Best Local Similarity   94.7%;  Pred. No. 7.2e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 tgtggagcctcaacatcct 20
           ||||||| ||||||||||||
Db     171 TGTGGAGGCTCAACATCCT 153


RESULT   6
AQ605972
LOCUS       AQ605972                393 bp    DNA     linear   GSS 10-JUN-1999
DEFINITION  HS_5383_A2_C02_SP6E RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=959 Col=4 Row=E, DNA sequence.
ACCESSION   AQ605972
VERSION     AQ605972.1  GI:5065966
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 393)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
```

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           Plate: 959  row: E  column: 4
           Seq primer: SP6
           Class: BAC ends
           High quality sequence stop: 393.
FEATURES             Location/Qualifiers
     source          1. .393
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=959 Col=4 Row=E"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /sex="male"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     Male blood DNA was isolated from one randomly chosen donor
                     and partially digested with a combination of EcoRI and
                     EcoRI Methylase. Size selected DNA was cloned into the
                     pBACe3.6 vector at EcoRI sites"
BASE COUNT       80 a    115 c     68 g    130 t
ORIGIN


  Query Match             82.9%;  Score 17.4;  DB 12;  Length 393;
  Best Local Similarity   94.7%;  Pred. No. 7.2e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 gtggagcctcaacatcctg 21
          ||||||||||||| |||||
Db    321 GTGGAGCCTCAACCTCCTG 339


RESULT   7
FR0004279
LOCUS       FR0004279               427 bp    DNA     linear   GSS 27-FEB-1997
DEFINITION  F.rubripes GSS sequence, clone 045H22aB2, genomic survey sequence.
ACCESSION   Z88062
VERSION     Z88062.1  GI:1884974
KEYWORDS    GSS; genome survey sequence.
SOURCE      Takifugu rubripes.
  ORGANISM  Takifugu rubripes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Takifugu.
REFERENCE   1  (bases 1 to 427)
  AUTHORS   Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
            Williams,G. and Brenner,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource
            Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
COMMENT     Vector: m13mp18
            V_type: phage
            PRIMER: M13
            DESCR:
            One pass dye-terminator sequencing of cosmid cloned genomic
            sequence.
FEATURES             Location/Qualifiers
     source          1. .427
                     /organism="Takifugu rubripes"
                     /db_xref="taxon:31033"
                     /clone_lib="cosmid 045H22"
                     /clone="045H22aB2"
BASE COUNT      114 a    106 c     97 g    108 t      2 others
ORIGIN


  Query Match             82.9%;  Score 17.4;  DB 12;  Length 427;
  Best Local Similarity   94.7%;  Pred. No. 7.4e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 tgtggagcctcaacatcct 20
          ||||||| ||||||||||
Db    142 TGTGGAGGCTCAACATCCT 160


RESULT   8
AA851662/c
LOCUS       AA851662                534 bp    mRNA    linear   EST 30-APR-1998
DEFINITION  EST194430 Normalized rat placenta, Bento Soares Rattus sp. cDNA
            clone RPLAL16 3' end, mRNA sequence.
ACCESSION   AA851662
VERSION     AA851662.1  GI:2939202
KEYWORDS    EST.
SOURCE      Rattus sp.
  ORGANISM  Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 534)
  AUTHORS   Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
            Kerlavage,A.R. and Adams,M.D.
  TITLE     Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
            Gene Index
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Lee, NH
            The Institute for Genomic Research
            9712, Medical Center Drive, Rockville, MD 20850, USA
            Tel: (301)-838-3529
            Fax: (301)-838-0208
            Email: nhlee@tigr.org
            Seq primer: M13-21.
FEATURES             Location/Qualifiers
     source          1. .534
                     /organism="Rattus sp."
                     /db_xref="ATCC (inhost):2011580"
                     /db_xref="taxon:10118"
                     /clone="RPLAL16"
                     /clone_lib="Normalized rat placenta, Bento Soares"
                     /note="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI;
                     Site_2: NotI"
BASE COUNT      154 a    104 c    116 g    160 t
ORIGIN


  Query Match             82.9%;  Score 17.4;  DB 9;  Length 534;
  Best Local Similarity   94.7%;  Pred. No. 8e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 tgtggagcctcaacatcct 20
          ||||||||||||||| ||||
Db    500 TGTGGAGCCTCAACGTCCT 482


RESULT   9
FR0004290/c
LOCUS       FR0004290               619 bp    DNA     linear   GSS 27-FEB-1997
DEFINITION  F.rubripes GSS sequence, clone 045H22aA10, genomic survey sequence.
ACCESSION   Z88073
VERSION     Z88073.1  GI:1884985
KEYWORDS    GSS; genome survey sequence.
SOURCE      Takifugu rubripes.
  ORGANISM  Takifugu rubripes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Takifugu.
REFERENCE   1  (bases 1 to 619)
  AUTHORS   Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
            Williams,G. and Brenner,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource
            Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
COMMENT     Vector: m13mp18
            V_type: phage
            PRIMER: M13
            DESCR:
            One pass dye-terminator sequencing of cosmid cloned genomic
            sequence.
```

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FEATURES             Location/Qualifiers
     source          1. .619
                     /organism="Takifugu rubripes"
                     /db_xref="taxon:31033"
                     /clone_lib="cosmid 045H22"
                     /clone="045H22aA10"
BASE COUNT      160 a    160 c    140 g    157 t      2 others
ORIGIN


  Query Match             82.9%;  Score 17.4;  DB 12;  Length 619;
  Best Local Similarity   94.7%;  Pred. No. 8.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 tgtggagcctcaacatcct 20
          ||||||| ||||||||||
Db    206 TGTGGAGGCTCAACATCCT 188


RESULT  10
FR0004298/c
LOCUS       FR0004298               619 bp    DNA     linear   GSS 27-FEB-1997
DEFINITION  F.rubripes GSS sequence, clone 045H22aE3, genomic survey sequence.
ACCESSION   Z88081
VERSION     Z88081.1  GI:1884993
KEYWORDS    GSS; genome survey sequence.
SOURCE      Takifugu rubripes.
  ORGANISM  Takifugu rubripes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Takifugu.
REFERENCE   1  (bases 1 to 619)
  AUTHORS   Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
            Williams,G. and Brenner,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource
            Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
COMMENT     Vector: m13mp18
            V_type: phage
            PRIMER: M13
            DESCR:
            One pass dye-terminator sequencing of cosmid cloned genomic
            sequence.
FEATURES             Location/Qualifiers
     source          1. .619
                     /organism="Takifugu rubripes"
                     /db_xref="taxon:31033"
                     /clone_lib="cosmid 045H22"
                     /clone="045H22aE3"
BASE COUNT      153 a    149 c    143 g    158 t     16 others
ORIGIN


  Query Match             82.9%;  Score 17.4;  DB 12;  Length 619;
  Best Local Similarity   94.7%;  Pred. No. 8.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 tgtggagcctcaacatcct 20
          ||||||| ||||||||||
Db    403 TGTGGAGGCTCAACATCCT 385


RESULT  11
FR0004319/c
LOCUS       FR0004319               619 bp    DNA     linear   GSS 27-FEB-1997
DEFINITION  F.rubripes GSS sequence, clone 045H22aE5, genomic survey sequence.
ACCESSION   Z88102
VERSION     Z88102.1  GI:1885014
KEYWORDS    GSS; genome survey sequence.
SOURCE      Takifugu rubripes.
  ORGANISM  Takifugu rubripes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Takifugu.
REFERENCE   1  (bases 1 to 619)
  AUTHORS   Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
            Williams,G. and Brenner,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource
            Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
COMMENT     Vector: m13mp18
            V_type: phage
            PRIMER: M13
            DESCR:
            One pass dye-terminator sequencing of cosmid cloned genomic
            sequence.
FEATURES             Location/Qualifiers
     source          1. .619
                     /organism="Takifugu rubripes"
                     /db_xref="taxon:31033"
                     /clone_lib="cosmid 045H22"
                     /clone="045H22aE5"
BASE COUNT      163 a    161 c    129 g    153 t     13 others
ORIGIN


  Query Match             82.9%;  Score 17.4;  DB 12;  Length 619;
  Best Local Similarity   94.7%;  Pred. No. 8.3e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 tgtggagcctcaacatcct 20
          ||||||| ||||||||||
Db    210 TGTGGAGGCTCAACATCCT 192


RESULT  12
BE876167
LOCUS       BE876167                651 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601485668F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888065 5',
            mRNA sequence.
ACCESSION   BE876167
VERSION     BE876167.1  GI:10324943
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 651)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9667  row: h  column: 18
            High quality sequence stop: 647.
FEATURES             Location/Qualifiers
     source          1. .651
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3888065"
                     /clone_lib="NIH_MGC_69"
                     /tissue_type="large cell carcinoma, undifferentiated"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.1 kb.   Library constructed by Life
                     Technologies."
```

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BASE COUNT      137 a    188 c    200 g    126 t
ORIGIN


  Query Match             82.9%;  Score 17.4;  DB 10;  Length 651;
  Best Local Similarity   94.7%;  Pred. No. 8.4e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 gtggagcctcaacatcctg 21
          ||||||| ||||||||||
Db    582 GTGGAGCTTCAACATCCTG 600


RESULT  13
BM029637/c
LOCUS       BM029637                 229 bp    mRNA    linear   EST 05-NOV-2001
DEFINITION  IpSkn02153 Skin cDNA library Ictalurus punctatus cDNA 5', mRNA
            sequence.
ACCESSION   BM029637
VERSION     BM029637.1  GI:16743207
KEYWORDS    EST.
SOURCE      channel catfish.
  ORGANISM  Ictalurus punctatus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
            Ictaluridae; Ictalurus.
REFERENCE   1  (bases 1 to 229)
  AUTHORS   Karsi,A., Cao,D., Li,P., Ju,Z., Kocabas,A., Feng,J., Patterson,A.,
            Mickett,K.D. and Liu,Z.
  TITLE     Transcriptome analysis of channel catfish (Ictalurus punctatus):
            Initial analysis of gene expression and microsatellite-containing
            cDNAs in the skin
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Liu ZJ
            The Fish Molecular Genetics and Biotechnology Laboratory,
            Department of Fisheries and Allied Aquacultures and Program of Cell
            and Molecular Biosciences
            Auburn University
            203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
            Tel: 334 844 4054
            Fax: 334 844 9208
            Email: zliu@acesag.auburn.edu
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .229
                     /organism="Ictalurus punctatus"
                     /db_xref="taxon:7998"
                     /clone_lib="Skin cDNA library"
                     /note="Organ: Skin; Vector: pSport1; Site_1: NotI; Site_2:
                     SalI"
BASE COUNT       68 a     59 c     49 g     53 t
ORIGIN


  Query Match             80.0%;  Score 16.8;  DB 10;  Length 229;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 gtgtggagcctcaacatcct 20
          |||||||| |||||||| ||
Db    154 GTGTGGAGACTCAACATGCT 135


RESULT  14
BB413927/c
LOCUS       BB413927                 291 bp    mRNA    linear   EST 16-JUL-2000
DEFINITION  BB413927 RIKEN full-length enriched, 7 days embryo Mus musculus
            cDNA clone C430035J15 3' similar to X04714 Human mRNA for
            apolipoprotein B-100 (apoB-100), mRNA sequence.
ACCESSION   BB413927
VERSION     BB413927.1  GI:9235282
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 291)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
            ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
            , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
            , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.
            , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
            ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.
            , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
            ,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .291
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="C430035J15"
                     /clone_lib="RIKEN full-length enriched, 7 days embryo"
                     /dev_stage="7 days embryo"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA
                     was cleaved with XhoI and BamHI. Vector: a modified
                     pBluescript KS(+) after bulk excision from Lambda FLC I."
BASE COUNT       79 a     83 c     40 g     89 t
ORIGIN


  Query Match             80.0%;  Score 16.8;  DB 9;  Length 291;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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```
Qy      1 gtgtggagcctcaacatcct 20
          ||||||||||||| | |||||
Db    107 GTGTGGAGCCTCGAGATCCT 88


RESULT  15
AA483942
LOCUS       AA483942                 297 bp    mRNA    linear   EST 15-AUG-1997
DEFINITION  ne92e08.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911750
            similar to contains Alu repetitive element;, mRNA sequence.
ACCESSION   AA483942
VERSION     AA483942.1  GI:2212755
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 297)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -41m13 fwd. ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .297
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:911750"
                     /clone_lib="NCI_CGAP_Kid1"
                     /tissue_type="kidney"
                     /lab_host="DH10B"
                     /note="Vector: pAMP10; mRNA made from invasive kidney
                     tumor, cDNA made by oligo-dT priming.  Non-directionally
                     cloned.  Size-selected on agarose gel, average insert
                     size 600 bp. Reference:  Krizman et al. (1996) Cancer
                     Research 56:5380-5383."
BASE COUNT       74 a     80 c     75 g     68 t
ORIGIN


  Query Match             80.0%;  Score 16.8;  DB 9;  Length 297;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 tgtggagcctcaacatcctg 21
          |||| ||||||||| |||||
Db     46 TGTGCAGCCTCAACCTCCTG 65


Search completed: July 16, 2002, 09:20:48
Job time: 7401 sec
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Hashemi, S.
09/981606

FILE 'REGISTRY' ENTERED AT 11:51:27 ON 16 JUL 2002
L1 22 S GTGTGGAGCCTCAACATCCTG/SQSN

FILE 'HCAPLUS' ENTERED AT 11:59:04 ON 16 JUL 2002
L2 5 S L1

L2 ANSWER 1 OF 5 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:769079 HCAPLUS
DOCUMENT NUMBER: 133:318316
TITLE: Hereditary hemochromatosis genes and their protein products and mutations
INVENTOR(S): Thomas, Winston J.; Drayna, Dennis T.; Feder, John N.; Gnirke, Andreas; Ruddy, David; Tsuchihashi, Zenta; Wolff, Roger K.
PATENT ASSIGNEE(S): Bio-Rad Laboratories, Inc., USA
SOURCE: U.S., 108 pp., Cont.-in-part of U.S. Ser. No. 630,912, abandoned.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 6
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6140305	A	20001031	US 1997-834497	19970404
US 5712098	A	19980127	US 1996-632673	19960416
US 6025130	A	20000215	US 1996-652265	19960523

PRIORITY APPLN. INFO.: US 1996-630912 B2 19960404
US 1996-632673 A2 19960416
US 1996-652265 A2 19960523

AB The invention relates generally to the gene, and mutations thereto, that are responsible for the disease hereditary hemochromatosis (HH). More particularly, the invention relates to the identification, isolation, and cloning of the DNA sequence corresponding to the normal and mutant HH genes, as well as the characterization of their transcripts and gene products. The invention also related to methods and the like for screening for HH homozygotes and further relates to HH diagnosis, prenatal screening and diagnosis, and therapies of HH disease, including gene therapeutics, protein and antibody based therapeutics, and small mol. therapeutics.

IT **198653-27-9 257856-52-3 257856-53-4**
257856-54-5
RL: ADV (Adverse effect, including toxicity); BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(nucleotide sequence; hereditary hemochromatosis genes and their protein products and mutations)

REFERENCE COUNT: 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 2 OF 5 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:707334 HCAPLUS
DOCUMENT NUMBER: 133:280150
TITLE: Novel mutations in the HFE gene associated with

iron storage disorders including hemochromatosis
INVENTOR(S): Rothenberg, Barry E.; Sawada-Hirai, Ritsuko; Barton, James C.
PATENT ASSIGNEE(S): Billups-Rothenberg, Inc., USA
SOURCE: PCT Int. Appl., 55 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000058515	A1	20001005	WO 2000-US7982	20000324
W: AU, CA, JP, NZ, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 6355425	B1	20020312	US 1999-277457	19990326
EP 1165840	A1	20020102	EP 2000-919650	20000324
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRIORITY APPLN. INFO.: US 1999-277457 A1 19990326
WO 2000-US7982 W 20000324

AB The invention features a method of diagnosing an iron disorder, e.g., hemochromatosis, or a genetic susceptibility to developing such a disorder in a mammal by detg. the presence of a mutation in exon 2 or in an intron of an HFE acid. New mutations in the HFE gene encoding the HLA-H antigen and involved in the etiol. of iron storage diseases such as hemochromatosis are described for use in diagnosis. Primers and probes for detection of these mutations are described.

IT **187501-78-6**, GenBank Z92910
RL: ANT (Analyte); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence, detection of mutation in; novel mutations in HFE gene assocd. with iron storage disorders including hemochromatosis)

IT **299247-30-6**
RL: PRP (Properties)
(unclaimed sequence; novel mutations in the HFE gene assocd. with iron storage disorders including hemochromatosis)

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 3 OF 5 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:114386 HCAPLUS
DOCUMENT NUMBER: 132:150279
TITLE: The gene involved in hereditary hemochromatosis and its diagnostic and therapeutic uses
INVENTOR(S): Thomas, Winston J.; Drayna, Dennis T.; Feder, John N.; Gnirke, Andreas; Ruddy, David; Tsuchihashi, Zenta; Wolff, Roger K.
PATENT ASSIGNEE(S): Mercator Genetics, Inc., USA
SOURCE: U.S., 91 pp., Cont.-in-part of U.S. Ser. No. 632,673.
CODEN: USXXAM
DOCUMENT TYPE: Patent

LANGUAGE: English
FAMILY ACC. NUM. COUNT: 6
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6025130	A	20000215	US 1996-652265	19960523
US 5712098	A	19980127	US 1996-632673	19960416
US 5872237	A	19990216	US 1996-724394	19961001
WO 9738137	A1	19971016	WO 1997-US6254	19970404
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, US, US, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9726701	A1	19971029	AU 1997-26701	19970404
AU 733459	B2	20010517		
EP 954602	A1	19991110	EP 1997-918642	19970404
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
US 6140305	A	20001031	US 1997-834497	19970404
US 6228594	B1	20010508	US 2000-503444	20000214

PRIORITY APPLN. INFO.:
US 1996-630912 B2 19960404
US 1996-632673 A2 19960416
US 1996-652265 A2 19960523
WO 1997-US6254 W 19970404

AB The HH gene that is mutated in the disease hereditary hemochromatosis (HH) is cloned and wild-type and mutant alleles assocd. with the disease are characterized. In addn., the gene products of these alleles are characterized. The invention also relates to methods and the like for screening for HH homozygotes for diagnosis, prenatal screening and diagnosis, treatment of the disease, including gene therapy, protein and antibody based therapy, and small mol. therapeutics. The gene product is similar to an MHC mol. but the gene, which maps close to the MHC cluster on chromosome 6p, does not show the polymorphism typical of member of the MHC family.

IT **198653-27-9**, DNA (human hereditary hemochromatosis gene plus flanks) **257856-52-3 257856-53-4**
257856-54-5
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(nucleotide sequence; gene involved in hereditary hemochromatosis and its diagnostic and therapeutic uses)

REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 4 OF 5 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1998:228028 HCAPLUS
DOCUMENT NUMBER: 129:1219
TITLE: The haemochromatosis candidate gene HFE (HLA-H) of man and mouse is located in syntenic regions

within the histone gene cluster

AUTHOR(S): Albig, Werner; Drabent, Birgit; Burmester, Nicole; Bode, Christa; Doenecke, Detlef

CORPORATE SOURCE: Institut fur Biochemie und Molekulare Zellbiologie, Universitat Gottingen, Gottingen, Germany

SOURCE: Journal of Cellular Biochemistry (1998), 69(2), 117-126
CODEN: JCEBD5; ISSN: 0730-2312
PUBLISHER: Wiley-Liss, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The HFE (HLA-H) gene is a strong candidate gene for hereditary hemochromatosis and was localized on the short arm of chromosome 6 to 6p21.3-p22. In addn., the sequence of the homologous mouse and rat cDNA and a partial sequence from the mouse gene have been reported recently. In this report, we describe the location of the human and the mouse HFE (HLA-H) gene within the histone gene clusters on the human chromosome 6 and the mouse chromosome 13. Both the human and the murine gene were located on syntenic regions within the histone gene clusters in the vicinity of the histone Hit gene. The genomic sequence of the human HFE (HLA-H) gene and the 3' portion of the homologous mouse gene were detd. Comparison of the genomic sequences from man and mouse and the cDNA sequence from rat shows significant similarities, also beyond the transcribed region of the mouse gene.

IT **187501-78-6**, DNA (human clone ICRFy901D1223 gene HFE)
RL: PRP (Properties)
(nucleotide sequence; hemochromatosis candidate gene HFE (HLA-H) of man and mouse is located in syntenic regions within the histone gene cluster)

L2 ANSWER 5 OF 5 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1997:684528 HCAPLUS
DOCUMENT NUMBER: 127:355966
TITLE: Cloning and sequencing of hereditary hemochromatosis gene with therapeutic and diagnostic approaches for disease treatment

INVENTOR(S): Thomas, Winston J.; Drayna, Dennis T.; Feder, John N.; Gnirke, Andreas; Ruddy, David; Tsuchihashi, Zenta; Wolff, Roger K.

PATENT ASSIGNEE(S): Mercator Genetics, Inc., USA; Thomas, Winston J.; Drayna, Dennis T.; Feder, John N.; Gnirke, Andreas; Ruddy, David; Tsuchihashi, Zenta; Wolff, Roger K.

SOURCE: PCT Int. Appl., 114 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 6

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9738137	A1	19971016	WO 1997-US6254	19970404

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX,

NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT,
UA, UG, US, US, US, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU,
TJ, TM
RW: GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR,
GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM,
GA, GN, ML, MR, NE, SN, TD, TG

US 5712098	A	19980127	US 1996-632673	19960416
US 6025130	A	20000215	US 1996-652265	19960523
AU 9726701	A1	19971029	AU 1997-26701	19970404
AU 733459	B2	20010517		
EP 954602	A1	19991110	EP 1997-918642	19970404

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,
PT, IE, FI

PRIORITY APPLN. INFO.:

US 1996-630912	A2	19960404
US 1996-632673	A2	19960416
US 1996-652265	A2	19960523
WO 1997-US6254	W	19970404

AB The identification, isolation, and cloning of the DNA sequence, transcripts and gene products corresponding to the gene and mutations that are responsible for the disease hereditary hemochromatosis (HH) is presented. Methods are presented for PCR screening for HH homozygotes and further relates to HH diagnosis, prenatal screening and diagnosis, and therapies of HH disease, including gene therapeutics, protein and antibody based therapeutics, and small mol. therapeutics.

IT **198653-27-9 198653-28-0 198653-29-1**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; cloning and sequencing of hereditary hemochromatosis gene with therapeutic and diagnostic approaches for disease treatment)

E1 THROUGH E8 ASSIGNED

FILE 'REGISTRY' ENTERED AT 12:00:23 ON 16 JUL 2002
L3 8 S E1-E8

L3 ANSWER 1 OF 8 REGISTRY COPYRIGHT 2002 ACS
RN **299247-30-6** REGISTRY
CN 13: PN: WO0058515 SEQID: 15 unclaimed sequence (9CI) (CA INDEX NAME)
SQL 21
MF Unspecified
CI MAN

REFERENCE 1: 133:280150

L3 ANSWER 2 OF 8 REGISTRY COPYRIGHT 2002 ACS
RN **257856-54-5** REGISTRY
CN DNA (human hereditary hemochromatosis gene allele 24d1 plus allele 24d2 plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 6: PN: US6025130 SEQID: 7 claimed DNA
CN 7: PN: US6140305 SEQID: 7 claimed DNA
SQL 10825
MF Unspecified
CI MAN

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REFERENCE 1: 133:318316

REFERENCE 2: 132:150279

L3 ANSWER 3 OF 8 REGISTRY COPYRIGHT 2002 ACS
RN **257856-53-4** REGISTRY
CN DNA (human hereditary hemochromatosis gene allele 24d2 plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 4: PN: US6025130 SEQID: 5 claimed DNA
CN 5: PN: US6140305 SEQID: 5 claimed DNA
SQL 10825
MF Unspecified
CI MAN

REFERENCE 1: 133:318316

REFERENCE 2: 132:150279

L3 ANSWER 4 OF 8 REGISTRY COPYRIGHT 2002 ACS
RN **257856-52-3** REGISTRY
CN DNA (human hereditary hemochromatosis gene allele 24d1 plus flanks) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 2: PN: US6025130 SEQID: 3 claimed DNA
CN 3: PN: US6140305 SEQID: 3 claimed DNA
SQL 10825
MF Unspecified
CI MAN

REFERENCE 1: 133:318316

REFERENCE 2: 132:150279

L3 ANSWER 5 OF 8 REGISTRY COPYRIGHT 2002 ACS
RN **198653-29-1** REGISTRY
CN DNA (human hereditary hemochromatosis gene 24d2 mutant plus flanks) (9CI) (CA INDEX NAME)
SQL 10824
MF Unspecified
CI MAN

REFERENCE 1: 127:355966

L3 ANSWER 6 OF 8 REGISTRY COPYRIGHT 2002 ACS
RN **198653-28-0** REGISTRY
CN DNA (human hereditary hemochromatosis gene 24d1 mutant plus flanks) (9CI) (CA INDEX NAME)
SQL 10824
MF Unspecified
CI MAN

REFERENCE 1: 127:355966

L3 ANSWER 7 OF 8 REGISTRY COPYRIGHT 2002 ACS
RN **198653-27-9** REGISTRY
CN DNA (human hereditary hemochromatosis gene plus flanks) (9CI) (CA INDEX NAME)

OTHER NAMES:
CN 1: PN: US6025130 SEQID: 1 claimed DNA
CN 1: PN: US6140305 SEQID: 1 claimed DNA
SQL 10824
MF Unspecified
CI MAN

REFERENCE 1: 133:318316

REFERENCE 2: 132:150279

FERENCE 3: 127:355966

L3 ANSWER 8 OF 8 REGISTRY COPYRIGHT 2002 ACS
RN **187501-78-6** REGISTRY
CN DNA (human clone ICRFy901D1223 gene HFE) (9CI) (CA INDEX NAME)
SQL 12146
MF Unspecified
CI MAN

REFERENCE 1: 133:280150

REFERENCE 2: 129:1219

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FILE 'HOME' ENTERED AT 12:00:43 ON 16 JUL 2002